

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 2, 2004, 14:21:01 ; Search time 22 Seconds
(without alignment)
434.648 Million cell updates/sec

Title: US-09-965-529-26

Perfect score: 1200

Sequence: 1 MKWVAPTRFVNSCCCLCH.....YDDATVNGAKKEPPPPVSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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6: /cgn2_6/ptodata/1/iaa/6D COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	769	64.1	162	4	US-09-152-060-63
2	714	59.5	137	4	US-09-152-060-97
3	553.5	46.1	233	4	US-09-886-319A-12
4	541.5	45.1	233	4	US-09-886-319A-11
5	417	34.8	87	4	US-09-152-060-98
6	175.5	14.6	262	3	US-08-889-425-2
7	156	13.0	261	3	US-08-889-425-4
8	95	7.9	1872	6	5386025-6
9	95	7.9	1873	1	US-08-435-675B-4
10	95	7.9	1873	1	US-08-336-257A-7
11	89	7.4	713	4	US-09-107-532A-4559
12	88.5	7.4	2161	1	US-07-745-206A-2
13	88.5	7.4	2161	1	US-08-455-543A-49
14	88.5	7.4	2161	1	US-08-455-543A-51
15	88.5	7.4	2161	2	US-08-223-305C-49
16	88.5	7.4	2161	2	US-08-223-305C-51
17	88.5	7.4	2161	2	US-08-311-363-2
18	87.5	7.3	451	1	US-08-191-337-3
19	87.5	7.3	548	4	US-09-328-352-6605
20	86.5	7.2	241	4	US-09-107-532A-5558
21	85.5	7.1	667	3	US-08-959-004-11
22	83	6.9	775	4	US-09-252-991A-28461
23	83	6.9	870	4	US-09-134-001C-4959
24	82.5	6.9	493	3	US-08-476-123-12
25	80	6.7	315	4	US-09-393-634-56
26	80	6.7	1968	1	US-07-745-206A-7
27	80	6.7	1968	1	US-08-455-543A-45

28	80	6.7	1968	2	US-08-223-305C-45	Sequence 45, Appli
29	80	6.7	1968	2	US-08-311-363-7	Sequence 7, Appli
30	79.5	6.6	120	3	US-09-188-930-180	Sequence 180, App
31	79.5	6.6	120	4	US-09-312-283C-180	Sequence 180, App
32	79.5	6.6	421	4	US-09-198-452A-932	Sequence 932, App
33	79	6.6	219	2	US-08-855-140-3	Sequence 3, Appli
34	79	6.6	219	2	US-08-807-044-3	Sequence 3, Appli
35	79	6.6	219	5	PCT-US91-04986-2	Sequence 2, Appli
36	79	6.6	226	4	US-09-694-094-1	Sequence 1, Appli
37	78.5	6.5	907	1	US-08-349-006-2	Sequence 2, Appli
38	78.5	6.5	907	3	US-08-804-439A-19	Sequence 19, Appli
39	78.5	6.5	907	3	US-08-720-229-19	Sequence 19, Appli
40	78.5	6.5	907	4	US-09-171-699-2	Sequence 2, Appli
41	78.5	6.5	907	5	PCT-US94-04180-2	Sequence 2, Appli
42	77.5	6.5	358	4	US-08-937-834-4	Sequence 4, Appli
43	76.5	6.4	309	4	US-09-393-634-49	Sequence 49, Appli
44	76.5	6.4	344	4	US-09-134-001C-4175	Sequence 4175, Ap
45	76.5	6.4	373	4	US-09-252-991A-26370	Sequence 26370, A

ALIGNMENTS

RESULT 1
US-09-152-060-63
; Sequence 63, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 63
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-63

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Best Local Similarity	99.3%;	Pred. No. 7.8e-74;		
Matches 146;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	MKWVAPTRFVNSCCCLCHVTRCTILLGVYLIINAVLLILLSALADPPQYNSFSEL	60	
Db	1	MKWVAPTRFVNSCCCLCHVTRCTILLGVYLIINAVLLILLSALADPPQYNSFSEL	60	
Qy	61	GGDFEFDDNMCTIAISLMLILICAMATYGAKQRAAWIIPFCQIFDFALNMLVAI	120	
Db	61	GGDFEFDDNMCTIAISLMLILICAMATYGAKQRAAWIIPFCQIFDFALNMLVAI	120	

Qy 121 TVLIYPSNIOEYIRQLPPNPFYRDDVM 147
Db 121 TVLIYPSNIOEYIRQLPPNPFYRDDVM 147

RESULT 2

US-09-152-060-97
; Sequence 97, Application US/09152060,
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152.060
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040.762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040.710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050.934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048.100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048.357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048.189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057.765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048.970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068.368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 97
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-97

Query Match 59.5%; Score 714; DB 4; Length 137;
Best Local Similarity 99.3%; Pred. No. 4.2e-68;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 RYNSNCCCLCHVTRGTILGWWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 68
Db 1 RYNSNCCCLCHVTRGTILGWWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 60
Qy 69 DANMCIAIAISLLMLICAMATYGAAYKORAAWIIPFCYQIFDFALNMLVAITVLIYPSN 128
Db 61 DANMCIAIAISLLMLICAMATYGAAYKORAAWIIPFCYQIFDFALNMLVAITVLIYPSN 120
Qy 129 IOEYIRQLPPNPFYRDD 145
Db 121 IOEYIRQLPPNPFYRDD 137

RESULT 3

US-09-886-319A-12
; Sequence 12, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically

; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886.319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-319A-12

Query Match 46.1%; Score 553.5; DB 4; Length 233;
Best Local Similarity 45.2%; Pred. No. 7.8e-51;
Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;
Qy 9 RYNSNCCCLCHVTRGTILGWWYLIINAVVLLILLSALADPD-----QY-----NFSS 57
Db 13 RYSTRCCGCHVTRGTIILGTWVWVLLMAILLTVETVTHPNSMPAVNIQYEVIGNYS 72
Qy 58 SELGGDFEFMDANMCIAIAISLLMLICAMATYGAAYKORAAWIIPFCYQIFDFALNML 117
Db 73 SERMAD-----NACVLFAVSVLMFTISSMLVYGATSYQVGMILIPFCYRLEDFVLSC 125
Qy 118 VAITVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCTCLVLIILFISILTFKGLVLSVW 177
Db 126 VAISSTYLPRIKEYLDQL--PDFPYKDDLLALDSSCLLFVLVFFALFIIFKAYLINCV 184
Qy 178 NCYRINGRNSDVLVY-VTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 185 NCYKYNRRNVPEIAYPAEPQYVLYPYEMA-VKMPEKEPPPPYVLP 233

RESULT 4

US-09-886-319A-11
; Sequence 11, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886.319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-886-319A-11

Query Match 45.1%; Score 541.5; DB 4; Length 233;
Best Local Similarity 44.8%; Pred. No. 1.5e-49;
Matches 103; Conservative 44; Mismatches 62; Indels 21; Gaps 6;
Qy 9 RYNSNCCCLCHVTRGTILGWWYLIINAVVLLILLSALADPD-----QY-----NFSS 57
Db 13 RYSTRCCGCHVTRGTIILGTWVWVLLMAILLTVETVTHPNSMPAVNIQYEVIGNYS 72

APPLICANT: Adra, Chaker N.
TITLE OF INVENTION: A Lysosomal-Associated Multispanning

	Query Watch	7.9%;	Score 95;	DB 1;	Length 1873;
	Best Local Similarity	24.0%;	Pred. No. 0.35,		
	Matches	46;	Conservative 31;	Mismatches 69;	Indels 46; Gaps 9
Qy	12 SNSCCLCCHRTGTTLLGWYLIINAVVLLILLSALA----	DPQYNFSSSELGGDFEFM	67		
	: : :	: : : :	: : :	:	:
Db	785 TNKVVLCH--RIVNATWP-TNFILLPILLSAALAAEDPIRAESVRNQILGYFD-	--	836		
Qy	68 DDANWCIAIASLMLICAMTAYKQRAAWIIPFCYQITDFAIIMLVAILTVLIYN	127			
	: : :	: : : :	: : :	:	:
Db	837 -----IAFTSVTFEVIWKMTYGAFHLKGS-----FCRNYPNI-LDLIIWVAVSILI---	881			

	Query Match	7.4%;	Score 89;	DB 4;	Length 713;
	Best Local Similarity	21.8%;	Pred. No. 0.45;		
	Matches " 52; Conservative	38;	Mismatches 80;	Indels 68;	Gaps 12;
Qy	26 ILGVVYLINAVLLILLSALADPDQYNFSSE-----LG-GDFEFMDANMCIAIA	77			
	: :	:	: :	: :	:
Dd	187 IVLVICYLSIFIVITII-----FAFSKMKETLKKMLGYSNFDTKDISIKELNL	237			
Qy	78 ISLMMLICAMATYGAYKGRAAWIIPFCYCQIDFPAFLNM-LVAITVLIYP-NSIQBYIRQ	135			
	: : :	:	: :	: :	:
Dd	238 FCSLIITFILSFIISLYGNENPFSLCSPHFHFIISFIISLVTSIHVSLSIKNYLKXN	297			

Qy 136 LPPNFPYRDDVMSVNTCLVLIIILLFISIIILTFKGYLISCV-----W-- 177
Db 298 SRP-----LKLN--LCILNICLFLSMIL-----LIIASTKVNIHNEAENNSLKYWER 343
Qy 178 --NCRY-----YINGRN-----SSVLVVTSTNDTTLVLPYDDATVNGAAKE 218
Db 344 TTNLYKTNITNQLNRNNTVBNYYLKKASKFPVYKIQNKYTFIIAPYNYATIQENKKE 401

RESULT 12
US-07-745-206A-2
; Sequence 2, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Plannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745,206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-745-206A-2

Query Match 7.4%; Score 88.5; DB 1; Length 2161;
Best Local Similarity 25.0%; Pred. No. 2;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy 21 VRTGTLGVWVLIINAVVLLIISALA-----DP-DQYNFSSSELG-GDREFFMDANNCI 74
Db 875 IRVGHKUNHITFTNLIVFIMUSSAALAEEDPIRSHSFNTILGVFDYAF----- 926
Qy 75 AIAISLLMILICAMATYGAYKQRAWIIPFCYQIFDFALNMLVAITVIYIPNSIQEYIR 134
Db 927 -TAIFTVEILL-KWTFCAFLHKA-----FCRNVFNL-LDMLVGVSLV----- 968
Qy 135 QLPNFPYRDDVMSVNTCLVLIIILLFISIIILTFKGYLISCV-----YLISSCVNVCYRYINGRNSDVL 192
Db 969 ----SFGIQSSAISVVKILRVLRPLRLRAINRAKGLKHVVQCQVFVAIRTI-----GNIM 1019
Qy 193 VYVT 196
Db 1020 IVTT 1023

RESULT 13

Query Match 7.4%; Score 88.5; DB 1; Length 2161;
Best Local Similarity 25.0%; Pred. No. 2;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

US-08-455-543A-49
; Sequence 49, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-455-543A-49


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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seigman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-223-305C-49

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Query Match          7.4%; Score 88.5; DB 2; Length 2161;
Best Local Similarity 25.0%; Pred.No.2;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

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Db 875 IRVGHKLINHIFTNLTILVFIULSSAALAEDEPIRSHSPNTILGYDYAF----- 926

Qy 75 AIAISLLMILICAMATYGAVKQRAAWIIPFFCYQIFDFAIINMLVAITVLIYPNSIQEYIR 134
Db 927 -TAIFTVEILL-KMTTFGAPLHKA-----FCRNYFNL-LDMLVVGSLV----- 968

Qy 135 QLPNFPYRDDVMSVNPTCLVLIILLFISILTPKG--YLISCVMNCYRYINGRNSDVL 192
Db 969 ----SFGIQSSAISVVKILRVLRPLRLRAINRAKGLKHVVQCQVFAIRTI-----GNIM 1019

Qy 193 VYVT 196
Db 1020 IVTT 1023

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Search completed: February 2, 2004, 14:24:17
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: February 2, 2004, 14:21:56 ; Search time 177 Seconds
(without alignments)
1161.817 Million cell updates/sec

Title: US-09-965-529-26
Perfect score: 1200
Sequence: 1 MKMVAPWTRFYSNCCLCCH.....YDDATVNGAAKEPPPPYVSA 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
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8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
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15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
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21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep.*
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25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
31: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	226	1	PCT-US01-16450-1994
					Sequence 1994, Ap

2	1200	100.0	226	1	PCT-US01-16450A-1994
3	1200	100.0	226	18	US-09-488-725A-2720
4	1200	100.0	226	20	US-09-611-523-2
5	1200	100.0	226	20	US-09-641-377-412
6	1200	100.0	226	21	US-09-743-247A-92
7	1200	100.0	226	25	US-09-965-529-26
8	1200	100.0	226	25	US-09-969-680A-26
9	1200	100.0	226	26	US-10-069-034-26
10	1200	100.0	226	27	US-10-126-052A-381
11	1200	100.0	226	28	US-10-258-898A-2720
12	1200	100.0	226	28	US-10-264-237-1994
13	1200	100.0	226	28	US-10-286-897-2720
14	1200	100.0	226	29	US-10-305-278-2
15	1200	100.0	231	18	US-09-488-725A-6292
16	1200	100.0	231	28	US-10-258-898A-6292
17	1200	100.0	231	28	US-10-286-897-6292
18	1200	100.0	254	1	PCT-US02-19592-125
19	1200	100.0	254	27	US-10-177-488-125
20	1200	100.0	283	1	PCT-US01-42950-364
21	1200	100.0	283	1	PCT-US02-07826-175
22	1200	100.0	283	1	PCT-US02-19592-124
23	1200	100.0	283	1	PCT-US02-37431-99
24	1200	100.0	283	26	US-10-097-340-175
25	1200	100.0	283	27	US-10-177-488-124
26	1200	100.0	283	29	US-10-301-822-99
27	1200	100.0	283	30	US-10-416-993-364
28	892.5	74.4	301	1	PCT-US01-08656-6669
29	892.5	74.4	301	28	US-10-273-573-6669
30	769	64.1	162	23	US-09-852-659-63
31	769	64.1	162	23	US-09-852-659A-63
32	769	64.1	162	23	US-09-852-797-63
33	769	64.1	162	23	US-09-853-161-63
34	769	64.1	162	26	US-10-058-993-63
35	714	59.5	137	23	US-09-852-659-97
36	714	59.5	137	23	US-09-852-659A-97
37	714	59.5	137	23	US-09-852-797-97
38	714	59.5	137	23	US-09-853-161-97
39	714	59.5	137	26	US-10-058-993-97
40	682	56.8	157	20	US-09-673-840A-244
41	553.5	46.1	221	20	US-09-641-377-413
42	553.5	46.1	233	1	PCT-US01-16450-2149
43	553.5	46.1	233	1	PCT-US01-16450A-2149
44	553.5	46.1	233	28	US-10-264-237-2149
45	553.5	46.1	233	29	US-10-376-564-12

ALIGNMENTS

RESULT 1
PCT-US01-16450-1994
; Sequence 1994, Application PC/TUS0116450
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA131PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1994
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-16450-1994

Query Match 100.0%; Score 1200; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MKMVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVLLILLSALADPPQNPSSSEL 60

Db 1 MKVAPWTRFYSNCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIEDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIEDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLFISILITFKGYLISCVNVCY 180
Db 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLFISILITFKGYLISCVNVCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 2

PCT-US01-16450A-1994
; Sequence 1994, Application PC/TUS0116450A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P4131PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16450A
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1994
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-16450A-1994

Query Match 100.0%; Score 1200; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKVAPWTRFYSNCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Db 1 MKVAPWTRFYSNCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIEDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIEDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLFISILITFKGYLISCVNVCY 180
Db 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLFISILITFKGYLISCVNVCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 3

US-09-488-725A-2720
; Sequence 2720, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784F1PCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: PC_FL_genes_b Versions 1.0
; SEQ ID NO 2720
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2720

Query Match 100.0%; Score 1200; DB 18; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKVAPWTRFYSNCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Db 1 MKVAPWTRFYSNCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIEDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIEDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLFISILITFKGYLISCVNVCY 180
Db 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLFISILITFKGYLISCVNVCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 4

US-09-611-523-2
; Sequence 2, Application US/09611523
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: KAWAI, YURI
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: HAYASHI, KOJI
; TITLE OF INVENTION: SECRETORY PROTEIN OR MEMBRANE PROTEIN
; FILE REFERENCE: 084335/0121
; CURRENT APPLICATION NUMBER: US/09/611,523
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 1999-194179
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: JP 2000-118775
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183766
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/159,586
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,323
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 679
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-611-523-2

Query Match 100.0%; Score 1200; DB 20; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Qy 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILLTFKGYLISCWVNCY 180
Db 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILLTFKGYLISCWVNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226

RESULT 5

US-09-641-377-412
; Sequence 412, Application US/09641377
; GENERAL INFORMATION:
; APPLICANT: WIEMANN, STEFAN
; APPLICANT: GASSENHUBER, JOHANN
; APPLICANT: TAMPE, JENS
; TITLE OF INVENTION: HUMAN DNA SEQUENCES
; FILE REFERENCE: 087100/0106
; CURRENT APPLICATION NUMBER: US/09/641,377
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,499
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/156,503
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 1793
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 412
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-377-412

Query Match 100.0%; Score 1200; DB 20; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Qy 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILLTFKGYLISCWVNCY 180
Db 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILLTFKGYLISCWVNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226

RESULT 6

US-09-743-247A-92
; Sequence 92, Application US/09743247A
; GENERAL INFORMATION:
; APPLICANT: Sagami Chemical Research Center; Protegene Inc.
; TITLE OF INVENTION: Human Proteins Having Hydrophobic Domains And DNAs Encoding These
; FILE REFERENCE: 1997.13300
; CURRENT APPLICATION NUMBER: US/09/743,247A
; CURRENT FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: JP 10-208820
; PRIOR FILING DATE: 1998-07-24

; PRIOR APPLICATION NUMBER: JP 10-224105
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: JP 10-238116
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: JP 10-254736
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: JP 10-275505
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Windows 95 (Word 98)
; SEQ ID NO 92
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-743-247A-92

Query Match 100.0%; Score 1200; DB 21; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Qy 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILLTFKGYLISCWVNCY 180
Db 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILLTFKGYLISCWVNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226

RESULT 7

US-09-965-529-26
; Sequence 26, Application US/09965529
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PP-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 26
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2795577CDI
US-09-965-529-26

Query Match 100.0%; Score 1200; DB 25; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60

Db 1 MKWVAPWTRFYNSCCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDFFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 61 GGDFFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Qy 121 TVLIYFNSIQEYIRQLPFPYRDDVMSVNPCTCLVLIILFISILITFKGYLISCVWNCY 180
Db 121 TVLIYFNSIQEYIRQLPFPYRDDVMSVNPCTCLVLIILFISILITFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 8

US-09-969-680A-26

; Sequence 26, Application US/09969680A

; GENERAL INFORMATION:

; APPLICANT: LAL, Preeti; YUE, Henry

; APPLICANT: TANG, Y. Tom; BANDMAN, Olga

; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda

; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.

; APPLICANT: PATTERSON, Chandra

; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS

; FILE REFERENCE: PP-0731-1 USA

; CURRENT APPLICATION NUMBER: US/09/969,680A

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US000/22315

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/149,641

; PRIOR FILING DATE: 1999-08-17

; PRIOR APPLICATION NUMBER: 60/164,203

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PERL Program

; SEQ ID NO 26

; LENGTH: 226

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: 2795577CD1

US-09-969-680A-26

Query Match 100.0%; Score 1200; DB 25; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYNSCCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDFFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 61 GGDFFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Qy 121 TVLIYFNSIQEYIRQLPFPYRDDVMSVNPCTCLVLIILFISILITFKGYLISCVWNCY 180
Db 121 TVLIYFNSIQEYIRQLPFPYRDDVMSVNPCTCLVLIILFISILITFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 9

US-10-069-034-26

; Sequence 26, Application US/10069034

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: LAL, Preeti

; APPLICANT: YUE, Henry

; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PP-0731 PCT
; CURRENT APPLICATION NUMBER: US/10/069,034
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203
; PRIOR FILING DATE: 1999-08-17; 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 26
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2795577CD1
US-10-069-034-26

Query Match 100.0%; Score 1200; DB 26; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYNSCCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDFFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 61 GGDFFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Qy 121 TVLIYFNSIQEYIRQLPFPYRDDVMSVNPCTCLVLIILFISILITFKGYLISCVWNCY 180
Db 121 TVLIYFNSIQEYIRQLPFPYRDDVMSVNPCTCLVLIILFISILITFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 10

US-10-126-052A-381

; Sequence 381, Application US/10126052A

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Murray, Richard

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and

; FILE REFERENCE: 018501-001530US

; CURRENT APPLICATION NUMBER: US/10/126,052A

; CURRENT FILING DATE: 2002-04-18

; PRIOR APPLICATION NUMBER: US 60/284,770

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: US 60/290,492

; PRIOR FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: US 60/339,245

; PRIOR FILING DATE: 2001-11-09

; PRIOR APPLICATION NUMBER: US 60/350,666

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/334,370

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: US 60/372,246

; PRIOR FILING DATE: 2002-04-12

; NUMBER OF SEQ ID NOS: 691

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 381

; LENGTH: 226

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-126-052A-381

Query Match      100.0%; Score 1200; DB 27; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWAPWTRFYNSCCCLCHVTRGTILLGWYLIINAVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWAPWTRFYNSCCCLCHVTRGTILLGWYLIINAVLLILLSALADPPQYNFSSSEL 60

Qy 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPSNIOBYIRQLPFPNPPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPSNIOBYIRQLPFPNPPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180

Qy 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 11
US-10-258-898A-2720
; Sequence 2720, Application US/10258898A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/258,898A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 2720
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-898A-2720

Query Match      100.0%; Score 1200; DB 28; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWAPWTRFYNSCCCLCHVTRGTILLGWYLIINAVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWAPWTRFYNSCCCLCHVTRGTILLGWYLIINAVLLILLSALADPPQYNFSSSEL 60

Qy 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPSNIOBYIRQLPFPNPPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPSNIOBYIRQLPFPNPPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180

Qy 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 12
US-10-264-237-1994
; Sequence 1994, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAI31P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1994
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-1994

Query Match      100.0%; Score 1200; DB 28; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWAPWTRFYNSCCCLCHVTRGTILLGWYLIINAVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWAPWTRFYNSCCCLCHVTRGTILLGWYLIINAVLLILLSALADPPQYNFSSSEL 60

Qy 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPSNIOBYIRQLPFPNPPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPSNIOBYIRQLPFPNPPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180

Qy 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 13
US-10-286-897-2720
; Sequence 2720, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/286,897
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
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; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 2720
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-897-2720

Query Match      100.0%; Score 1200; DB 28; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60

Qy 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

; RESULT 14
US-10-305-278-2
; Sequence 2, Application US/10305278
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: KAWAI, YURI
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: HAYASHI, KOJI
; TITLE OF INVENTION: SECRETORY PROTEIN OR MEMBRANE PROTEIN
; FILE REFERENCE: 084335/0121
; CURRENT APPLICATION NUMBER: US/10/305,278
; CURRENT FILING DATE: 2002-11-27
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 1999-07-08
; PRIOR FILING DATE: 1999-07-08
; PRIOR FILING DATE: 2000-01-11
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 1999-10-18
; PRIOR FILING DATE: 1999-10-18
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 679
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-305-278-2

Query Match      100.0%; Score 1200; DB 29; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60

Qy 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120

; RESULT 15
US-09-488-725A-6292
; Sequence 6292, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 6292
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6292

Query Match      100.0%; Score 1200; DB 18; Length 231;
Best Local Similarity 100.0%; Pred. No. 4.9e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 6 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 65

Qy 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 66 GGDPEFMDANMCIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 125

Qy 121 TVLIYPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 126 TVLIYPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 185

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 186 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 231

Search completed: February 2, 2004, 14:27:26
Job time : 179 secs
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OM protein - protein search, using sw model

Run on: February 2, 2004, 14:22:31 ; Search time 24 Seconds
(without alignments)
724.790 Million cell updates/sec

Title: US-09-965-529-26
Perfect score: 1200
Sequence: 1 MKWVAPWTRFYNSCLCCH.....YDDATVNGAAKEPPPPYVSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 370304 seqs, 76968869 residues

Total number of hits satisfying chosen parameters: 370304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending Patents AA New:*

1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
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7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	283	6	US-10-734-564-97
2	1200	100.0	317	6	US-10-700-439-119
3	1181	98.4	234	1	PCT-US03-38808-248
4	1161	96.8	233	1	PCT-US03-38808-240
5	1144	95.3	319	1	PCT-US03-38808-241
6	282.5	23.5	425	5	US-09-614-150A-36129
7	282.5	23.5	432	5	US-09-614-150A-4479
8	175.5	14.6	262	1	PCT-US02-41798A-33
9	153	12.8	205	1	PCT-US03-37278-7
10	122	10.2	165	5	US-09-614-150A-42447
11	101	8.4	260	6	US-10-415-182A-4106
12	97.5	8.1	1772	6	US-10-726-216-16
13	95	7.9	1873	6	US-10-726-216-22
14	94	7.8	250	5	US-09-614-150A-207
15	91	7.6	551	6	US-10-679-063-24094
16	89	7.4	241	5	US-09-614-150A-30138
17	89	7.4	1633	1	PCT-US03-30720-722
18	88.5	7.4	1755	6	US-10-322-696A-51
19	88.5	7.4	1755	6	US-10-322-696B-51
20	88.5	7.4	2166	6	US-10-726-216-4
21	88.5	7.4	2181	5	US-09-976-858-288
22	88.5	7.4	2181	6	US-10-322-696A-54
23	88.5	7.4	2181	6	US-10-726-216-18
24	88.5	7.4	2181	6	US-10-726-216-20
25	88.5	7.4	2181	6	US-10-322-696B-54
26	88	7.3	537	6	US-10-679-063-23292

27 7.3 1543 1 PCT-US03-33087-52 Sequence 52, Appl
28 7.2 1787 6 US-10-357-885-30 Sequence 30, Appl
29 85 7.1 492 6 US-10-739-930-10011 Sequence 10011, A
30 83 6.9 507 6 US-10-679-063-13232 Sequence 13232, A
31 83 6.9 507 6 US-10-679-063-15216 Sequence 15216, A
32 83 6.9 1854 6 US-10-726-216-2 Sequence 2, Appl
33 83 6.9 1873 1 PCT-US03-38193-1433 Sequence 1433, Ap
34 83 6.9 1873 6 US-10-357-885-28 Sequence 28, Appl
35 83 6.9 1873 6 US-10-723-860-1433 Sequence 1433, Ap
36 83 6.9 1873 6 US-10-726-216-12 Sequence 12, Appl
37 83 6.9 1873 6 US-10-726-216-14 Sequence 14, Appl
38 82 6.8 223 5 US-09-614-150A-19326 Sequence 19326, A
39 82 6.8 359 6 US-10-330-773-930 Sequence 930, App
40 82 6.8 451 6 US-10-425-114A-47648 Sequence 47648, A
41 81 6.8 513 5 US-09-614-150A-23358 Sequence 23358, A
42 80 6.7 277 6 US-10-472-928-3476 Sequence 3476, Ap
43 80 6.7 314 7 US-60-500-315-1114 Sequence 1114, Ap
44 80 6.7 315 6 US-10-364-861-56 Sequence 56, Appl
45 80 6.7 380 6 US-10-343-650A-288 Sequence 288, App

ALIGNMENTS

RESULT 1

US-10-734-564-97
; Sequence 97, Application US/10734564
; GENERAL INFORMATION:
; APPLICANT: Christopher C Burgess et al
; TITLE OF INVENTION: Detection Methods Using TIMP1
; FILE REFERENCE: 1657/2012
; CURRENT APPLICATION NUMBER: US/10/734.564
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-564-97

Query Match 100.0%; Score 1200; DB 6; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.1e-114;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKWVAPWTRFYNSCLCCHVRTGTLIGVYLIINAVLLILLSALADPPQYNSSEL	60
Db	58	MKWVAPWTRFYNSCLCCHVRTGTLIGVYLIINAVLLILLSALADPPQYNSSEL	117
Qy	61	GGDFEFDDANMCIAIAISLLMILICAMATYGAYKQRAAMIIPFCYQIFDFALNMLVAI	120
Db	118	GGDFEFDDANMCIAIAISLLMILICAMATYGAYKQRAAMIIPFCYQIFDFALNMLVAI	177
Qy	121	TVLIYPSNIEYIRQLPPNPYRDDVNSVNPCTLVLLIFLISILTFKGLVISCWNCY	180
Db	178	TVLIYPSNIEYIRQLPPNPYRDDVNSVNPCTLVLLIFLISILTFKGLVISCWNCY	237
Qy	181	RYINGRNSSDVLYVYTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA	226
Db	238	RYINGRNSSDVLYVYTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA	283

RESULT 2

US-10-700-439-119
; Sequence 119, Application US/10700439
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Burgess, Christopher
; APPLICANT: Myerow, Susan
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Maimonis, Peter
; APPLICANT: Molino, Gary

APPLICANT: Burtgart, Lawrence
APPLICANT: Boardman, Lisa A.
APPLICANT: Thibodeau, Steven
APPLICANT: Lewis, Marcia
TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
Biomarkers for Cancer
FILE REFERENCE: 1657/2022
CURRENT APPLICATION NUMBER: US/10/700,439
CURRENT FILING DATE: 2003-11-04
NUMBER OF SEQ ID NOS: 186
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 119
LENGTH: 317
TYPE: PRT
ORGANISM: Homo sapiens
US-10-700-439-119

Query Match 100.0%; Score 1200; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.4e-114;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 92 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 151
Qy 61 GGDPEFMDANMCIAISLMLICAMATYGAYKORAAWIIPFCYQIDPALNMLVAI 120
Db 152 GGDPEFMDANMCIAISLMLICAMATYGAYKORAAWIIPFCYQIDPALNMLVAI 211
Qy 121 TVLIYPNSIQEYIRQLPFPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 212 TVLIYPNSIQEYIRQLPFPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 271
Qy 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 272 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 317

RESULT 3

PCT-US03-38808-248

; Sequence 248, Application PC/TUS0338808

; GENERAL INFORMATION:

; APPLICANT: diadexus, Inc.

; APPLICANT: Macina, Roberto

; APPLICANT: Turner, Leah

; APPLICANT: Sun, Yongming

; APPLICANT: Rodriguez, Maria

; APPLICANT: Tim Burcham

; TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Colon Spec

; FILE REFERENCE: DEX-0450

; CURRENT APPLICATION NUMBER: PCT/US03/38808

; CURRENT FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: US 60/431,133

; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 254

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 248

; LENGTH: 234

; TYPE: PRT

; ORGANISM: Homo sapien

PCT-US03-38808-248

Query Match 98.4%; Score 1181; DB 1; Length 234;
Best Local Similarity 96.2%; Pred. No. 1.5e-112;
Matches 225; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

Qy 1 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Qy 61 GGDPEFMD-----ANMCIAISLMLICAMATYGAYKORAAWIIPFCYQIDF 112

Db 61 GGDPEFMDAKILFNLSADMCIAIAISLMLICAMATYGAYKORAAWIIPFCYQIDF 120
Qy 113 ALANMLVAITVLIYPNSIQEYIRQLPFPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYL 172
Db 121 ALANMLVAITVLIYPNSIQEYIRQLPFPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYL 180
Qy 173 ISCVWNCYRYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 ISCVWNCYRYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 234

RESULT 4

PCT-US03-38808-240

; Sequence 240, Application PC/TUS0338808

; GENERAL INFORMATION:

; APPLICANT: diadexus, Inc.

; APPLICANT: Macina, Roberto

; APPLICANT: Turner, Leah

; APPLICANT: Sun, Yongming

; APPLICANT: Rodriguez, Maria

; APPLICANT: Tim Burcham

; TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Colon Spec

; FILE REFERENCE: DEX-0450

; CURRENT APPLICATION NUMBER: PCT/US03/38808

; CURRENT FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: US 60/431,133

; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 254

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 240

; LENGTH: 233

; TYPE: PRT

; ORGANISM: Homo sapien

PCT-US03-38808-240

Query Match 96.8%; Score 1161; DB 1; Length 233;

Best Local Similarity 97.8%; Pred. No. 1.6e-110;

Matches 219; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Qy 61 GGDPEFMDANMCIAIAISLMLICAMATYGAYKORAAWIIPFCYQIDPALNMLVAI 120
Db 61 GGDPEFMDANMCIAIAISLMLICAMATYGAYKORAAWIIPFCYQIDPALNMLVAI 120
Qy 121 TVLIYPNSIQEYIRQLPFPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPNSIQEYIRQLPFPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYV 224
Db 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGACQCAPYV 224

RESULT 5

PCT-US03-38808-241

; Sequence 241, Application PC/TUS0338808

; GENERAL INFORMATION:

; APPLICANT: diadexus, Inc.

; APPLICANT: Macina, Roberto

; APPLICANT: Turner, Leah

; APPLICANT: Sun, Yongming

; APPLICANT: Rodriguez, Maria

; APPLICANT: Tim Burcham

; TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Colon Spec

; FILE REFERENCE: DEX-0450

; CURRENT APPLICATION NUMBER: PCT/US03/38808

; CURRENT FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: US 60/431,133

;; PRIOR FILING DATE: 2002-12-04
;; NUMBER OF SEQ ID NOS: 254
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 241
;; LENGTH: 319
;; TYPE: PRT
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (2)..(5)
;; OTHER INFORMATION: Xeany amino acid
PCT-US03-38808-241

Query Match 95.3%; Score 1144; DB 1; Length 319;
Best Local Similarity 98.2%; Pred. No. 1.2e-108;
Matches 216; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKWAPWTRFYSNCCCLCHVTRTGILLGVWYLIINAVVLLILSALADPDQYNFSSSEL 60
Db 85 MKWAPWTRFYSNCCCLCHVTRTGILLGVWYLIINAVVLLILSALADPDQYNFSSSEL 144
Qy 61 GGDFFMDANNCIAISLMLILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAI 120
Db 145 GGDFFMDANNCIAISLMLILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAI 204
Qy 121 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTPKGYLISCVWNCY 180
Db 205 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTPKGYLISCVWNCY 264
Qy 181 RYINGRNSDVLVYVTSNDTTLPPYDDATVNGAKPEPP 220
Db 265 RYINGRNSDVLVYVTSNDTTLPPYDDATVNGACQCAP 304

RESULT 6

US-09-614-150A-36129
; Sequence 36129, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.

;; CURRENT APPLICATION NUMBER: US/09/614,150A
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 36129
;; LENGTH: 425
;; TYPE: PRT
;; ORGANISM: DROSOPHILA
US-09-614-150A-36129

Query Match 23.5%; Score 282.5; DB 5; Length 425;
Best Local Similarity 26.4%; Pred. No. 9.2e-21;
Matches 68; Conservative 40; Mismatches 97; Indels 53; Gaps 5;

Qy 14 SCCLCCHVTRTGILLGVWYLIINAVVLLILSALADPDQYNFSSSEL-GGDFFEMDD--- 69
Db 32 TCCFGLVHTATLMIGLWHLFLNLIALSVLAVIWRNPEMMD-----ELEGGTHDVTDLISA 87
Qy 70 -----ANMCIAIAISLMLILICAMATYGAYKORAAWI 102
Db 88 PALPTPLSKVEPPYAYRDHSLNRYKRYQNFDMGGLVCTCMIAITLMMIYGTIKGKPSHLL 147
Qy 103 PFCYQIFDFALNMLVAITVLIVPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILF 162
Db 148 PFCYQIFDFALNMLVAITVLIVPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILF 206
Qy 163 SIILTPKGYLISCVWNCYRI-----NGRNSDVLVYVTSNDTTLVLLP 205
Db 207 ICIVFLKAYCIGIVMRCYKYLTLRQOHVTLFPPLPEPTGVHSGVGGTFGAERSYSTLLP 266
Qy 206 PYDDATVNGAKPEPPPY 223
Db 267 NYDEAIAQYLKQAPPPSY 284

RESULT 7

US-09-614-150A-4479
; Sequence 4479, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.

;; CURRENT APPLICATION NUMBER: US/09/614,150A
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4479
;; LENGTH: 432
;; TYPE: PRT
;; ORGANISM: DROSOPHILA
US-09-614-150A-4479

Query Match 23.5%; Score 282.5; DB 5; Length 432;
Best Local Similarity 26.4%; Pred. No. 9.4e-21;
Matches 68; Conservative 40; Mismatches 97; Indels 53; Gaps 5;

Qy 14 SCCLCCHVTRTGILLGVWYLIINAVVLLILSALADPDQYNFSSSEL-GGDFFEMDD--- 69
Db 39 TCCFGLVHTATLMIGLWHLFLNLIALSVLAVIWRNPEMMD-----ELEGGTHDVTDLISA 94
Qy 70 -----ANMCIAIAISLMLILICAMATYGAYKORAAWI 102
Db 95 PALPTPLSKVEPPYAYRDHSLNRYKRYQNFDMGGLVCTCMIAITLMMIYGTIKGKPSHLL 154
Qy 103 PFCYQIFDFALNMLVAITVLIVPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILF 162
Db 155 PFCYQIFDFALNMLVAITVLIVPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILF 213

Qy 163 SIILTFKYLISCWNCYRYI-----NGNSSDLVLYVTSNDTTVLLP 205
Db 214 ICIVFLKAYCTGIVWRCYKYLTLRQOHVRLFPFLPEPTGVHSGVGTGGAERYSYTLLP 273
Qy 206 PYDDATVNGAAKEPPPPY 223
Db 274 NYDEAIAQYLKQAPPPSY 291

RESULT 8
PCT-US02-41798A-33
; Sequence 33, Application PC/TUS0241798A
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P501481-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/41798A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 33
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapien

PCT-US02-41798A-33

Query Match 14.6%; Score 175.5; DB 1; Length 262;
Best Local Similarity 22.8%; Pred. No. 4.2e-10;
Matches 61; Conservative 48; Mismatches 83; Indels 75; Gaps 12;
Qy 14 SCCLCHVRTGTLGGVWYLIINAVVLLILLSALADPDQYVSSSELGGDFEFMDANMC 73
Db 11 TCC-CFNVRIATTALAIYHVIM-VSLLFIEHSEVAGKASCKLSQMG-----YLRADLI 64
Qy 74 IATAISLLMILICAMATYGAKQRAAWIIPFCYQIFDPALNMLVAITVLYPNSIQEYI 133
Db 65 SSFLITWLFISLSLLGVVKNREKYLPLFLSLQIMDYLLCLTLGSIYI---ELPAYL 121
Qy 134 -----ROLPNFPYR-----DDVMSVNPCTC----- 153
Db 122 KLASRSRASSKFFPLMTQLDLCFLSILTLCSYMEVPTYLNFKSMHNVLPQSDMPH 181
Qy 154 -----LVLTLLFISILTFKGYLISCWNCYRYINGNS-----SDLVVYVTSNDTT 201
Db 182 NQFIKMWIIFSIATITVLI-EKVYMFKCVWRCYKILCKMNSVEEKRNSKML-----QK 233

Qy 202 VLLPPYDDATVNGAAKEP-----PPPY 223
Db 234 VVLPSEYEEA-LSLPSKTPEGGPAPPY 259

RESULT 9
PCT-US03-37278-7
; Sequence 7, Application PC/TUS0337278
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; EMERLING, Brooke M.;
; APPLICANT: CHIEN, David; WANG, Jonathan T.;
; APPLICANT: RICHARDSON, Thomas W.; RAMKUMAR, Jayalaxmi;
; APPLICANT: KHARE, Reena; ELLIOTT, Vicki S.;
; APPLICANT: LEE, Soo Yeun; BHATIA, Umesh G.;
; APPLICANT: BURRILL, John D.; LEE, Sally;
; APPLICANT: BLAKE, Julie J.; HO, Anne;
; APPLICANT: ZHEN, Wenjin
; TITLE OF INVENTION: ORGANELLE-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1621 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/37278
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/429,445
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/430,833
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7522328CDI
PCT-US03-37278-7

Query Match 12.8%; Score 153; DB 1; Length 205;
Best Local Similarity 22.1%; Pred. No. 6.1e-08;
Matches 53; Conservative 42; Mismatches 67; Indels 78; Gaps 12;
Qy 14 SCCLCHVRTGTLGGVWYLIINAVVLLILLSALADPDQYVSSSELGGDFEFMDANMC 73
Db 11 TCC-CFNVRIATTALAIYHVNRKYLPLFL----- 39
Qy 74 IATAISLLMILICAMATYGAKQRAAWI-----IPFCYQIFDPALNMLVA-- 119
Db 40 ---SLQIMDYLLCLTLGSIYIELPAYLKLASRSRASSKFFPLMTQLDLCFLSILTLCS 96
Qy 120 --ITVLIYPN-SIQEYIROLP--PNFPYRDDVMSVNPCTCLVLIILLFISILTFKGYLIS 174
Db 97 SYMEVPTYLNFKSMHNVLPQSDMPHNOFI-----KMWIIFSIATITVLI-EKVYMFK 150
Qy 175 CVWNCYRYINGNS-----SDLVVYVTSNDTTVLLPPYDDATVNGAAKEP-----PPPY 223
Db 151 CVWRCYKILCKMNSVEEKRNSKML-----QKVLPSEYEEA-LSLPSKTPEGGPAPPY 202

RESULT 10
US-09-614-150A-42447
; Sequence 42447, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/09/614,150A
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19

OTHER INFORMATION: The 'Xaa' at location 390 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (391)..(391)
OTHER INFORMATION: The 'Xaa' at location 391 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (392)..(392)
OTHER INFORMATION: The 'Xaa' at location 392 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (393)..(393)
OTHER INFORMATION: The 'Xaa' at location 393 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (394)..(394)
OTHER INFORMATION: The 'Xaa' at location 394 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (395)..(395)
OTHER INFORMATION: The 'Xaa' at location 395 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (396)..(396)
OTHER INFORMATION: The 'Xaa' at location 396 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (397)..(397)
OTHER INFORMATION: The 'Xaa' at location 397 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (398)..(398)
OTHER INFORMATION: The 'Xaa' at location 398 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (399)..(399)
OTHER INFORMATION: The 'Xaa' at location 399 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (400)..(400)
OTHER INFORMATION: The 'Xaa' at location 400 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (401)..(401)
OTHER INFORMATION: The 'Xaa' at location 401 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (402)..(402)
OTHER INFORMATION: The 'Xaa' at location 402 stands for Lys, Asn, Arg, Ser, Thr,

OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (403)..(403)
OTHER INFORMATION: The 'Xaa' at location 403 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (404)..(404)
OTHER INFORMATION: The 'Xaa' at location 404 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (405)..(405)
OTHER INFORMATION: The 'Xaa' at location 405 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (406)..(406)
OTHER INFORMATION: The 'Xaa' at location 406 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (407)..(407)
OTHER INFORMATION: The 'Xaa' at location 407 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (408)..(408)
OTHER INFORMATION: The 'Xaa' at location 408 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (409)..(409)
OTHER INFORMATION: The 'Xaa' at location 409 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (410)..(410)
OTHER INFORMATION: The 'Xaa' at location 410 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (411)..(411)
OTHER INFORMATION: The 'Xaa' at location 411 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (412)..(412)
OTHER INFORMATION: The 'Xaa' at location 412 stands for Lys, Asn, Arg, Ser, Thr,
OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
OTHER INFORMATION: Cys, or Phe.
FEATURE:
NAME/KEY: misc feature

Query Match 8.1%; Score 97.5; DB 6; Length 1772;

Best Local Similarity 25.3%; Pred. No. 0.33;

Matches 47; Conservative 34; Mismatches 62; Indels 43; Gaps 10;

Oy 19 CHVRTGTLIGVWVLIINAVLILLSALA----DP-DQYVFSSEUG-GDFEFMDANM 72

Db 484 CRIVGCHKLNHIFNLILVIMLSAALAEEDPIRSHSFNTILGYDYAF-----537

Qy	73	CTAIAISLMLICAMATGYAYKORAWII	PFPCYQIFDFALANMLVAITVL	YIPNSIQBY	132
		: : :	: :		
Db	538	---TAITVEILL-KMTTFGAFLLHGA---	---FCRYFNLL-LDMLVVGVSLV---	---	579
Qy	133	IRQLPNNPYRDDVMVNPTCLVLII	LFISIIITPKG--YLISCVNVCYRYINGR	SSD	190
		: :	: :		
Db	580	-----SFGIOSSAISVVKILRVLRVLRPL	AINRAKGLKHVVQCVFAIRT	-----GN	628
Qy	191	VLVYVT	196		
		:::			
Db	629	IMIVTT	634		

```

RESULT 13
US-10-726-216-22
; Sequence 22, Application US/10726216
; GENERAL INFORMATION:
; APPLICANT: Nichols, Timothy C.
; APPLICANT: Malout, Nadia
; APPLICANT: Merricks, Elizabeth
; TITLE OF INVENTION: Purified and Isolated Platelet Calcium Channel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides and Therapeutic and Screening Methods Using Same
; FILE REFERENCE: 421/292/2
; CURRENT APPLICATION NUMBER: US/10726,216
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 09/029,413
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,169
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 1873
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-726-216-22

```

RESULT 14
US-09-614-150A-207
; Sequence 207, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/09/614,150A
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191

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; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 250
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-207

Query Match          7.8%; Score 94; DB 5; Length 250;
Best Local Similarity 19.9%; Pred. No. 0.079;
Matches 45; Conservative 37; Mismatches 78; Indels 66; Gaps 10;

Qy      3  MVAPWTRFFYSNCCCL--CC-----HVRTGTILLGVWYLIINAVVLLILLS 45
Db      1  MLLPTVSGSAAAGCKWNKCCRRSWEMLMAPVSPKNLRTTALTTSIYOLLISHCALFVLL 60
Qy      46  ALADPDQ-----YNPSSSELGGDFEFMDANNCIAIAISLMLICAM 88
Db      61  GLAHAEQMCVELELDILDQKNGFYNM--SPFHNDLRLQTAQAQAVATE-NLLYVMAGIA 117
Qy      89  ATY-----GAYKQRAAWIIPFCYQIFDFALNNLVAITVLIYPNISQEIYRIQLPPN 139
Db      118  GTYALSAIFLFFGVFXNRPGLIIPWL---VVEFIL--MIGLGALVFMLRDTKIYQLLGGQ 172
Qy      140  FPRYDDVMSVNPCLVLIILLFTSIILTF-KGYLIISCVWNCYRYIN 184
Db      173  VPY-----FICYILICMDYCKWYVMSFYOSLRMTN 204

```

```

RESULT 15
US-10-679-063-24094
; Sequence 24094, Application US/10679063
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCES: 38-15(52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 24094
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-679-063-24094

```

	Query Match	7.6%; Score 91; DB 6; Length 551;
	Best Local Similarity	22.0%; Pred. No. 0.39;
	Matches	37; Conservative 33; Mismatches 53; Indels 46; Gaps 9;
Qy	22 RTGTLLIGW-YLIINAVLIIILSALADPDQYNFSSELGGDFEFMDANMC-IATAIS	79
	: : : : : : : : : : : : : : : : : : :	
Dd	395 RSTPLIAVWTYAVLEIINLLGLA-----SSTAIGAVE-----NVCTVALNVS	438
Qy	80 LLMILICAMATYGAYKORAAWIIPFCYQIFDPAALMLVAITVLVIPNSIQEYIRQLPPN	139
	: : : : : : : : : : : : : : : : : : :	
Dd	439 YVPIICKM-VYGR-MQGGPWHMGKYSVVWNFAVAWNTFMVAFVF-----	482
Qy	140 FPYRDDVMVSNPTCLVLIILLFISIIILTFPKGYLISCVNVCNYINGRN	187

Db 483 PPTRVPPTENNVAIVVFFVLILALVF-----W-----YTHGRH 518

Search completed: February 2, 2004, 14:28:02
Job time : 26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2004, 14:20:15 ; Search time 21 Seconds
(without alignments)
1034.958 Million cell updates/sec

Title: US-09-965-529-26

Perfect score: 1200

Sequence: 1 MKVAVPTWTFYNSCLLCCH.....YDDATVNGAAKBPYPVSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175.5	14.6	262	2 G02476	lysosomal-associat
2	102.5	8.5	250	2 T15415	hypothetical prote
3	99.5	8.3	672	2 S52673	probable membrane
4	98.5	8.2	265	2 T26217	hypothetical prote
5	96	8.0	151	2 T18949	hypothetical prote
6	95	7.9	308	2 T20043	hypothetical prote
7	95	7.9	1873	2 A30063	dihydropyridine re
8	94.5	7.9	240	2 T15785	hypothetical prote
9	93.5	7.8	301	2 T21308	hypothetical prote
10	92.5	7.7	275	2 S41786	probable sugar tra
11	91.5	7.6	1032	2 H87470	AcR2/AcrD/AcrF fam
12	91	7.6	343	2 T14245	NADH2 dehydrogenas
13	89	7.4	391	2 A11762	hypothetical prote
14	88.5	7.4	1610	2 A46227	voltage-dependent
15	88.5	7.4	1646	2 JH0422	voltage-dependent
16	88.5	7.4	2161	2 JH0564	calcium channel al
17	88.5	7.4	2181	2 A38198	calcium channel al
18	88.5	7.4	2203	2 T42742	voltage-dependent
19	88	7.3	372	2 T24392	hypothetical prote
20	88	7.3	440	2 E89921	hypothetical prote
21	87.5	7.3	309	2 T24804	hypothetical prote
22	87.5	7.3	470	2 S47892	neutral amino acid
23	87.5	7.3	562	2 T26242	hypothetical prote
24	87	7.2	295	2 T32202	hypothetical prote
25	87	7.2	639	2 T50793	hypothetical prote
26	87	7.2	2220	2 A45290	calcium channel pr
27	85.5	7.1	667	2 A54915	EMP70 protein prec
28	85.5	7.1	757	2 C89473	protein F52D2.7 [i
29	85	7.1	254	2 T22339	hypothetical prote

30 85 7.1 347 2 S70364 cannabinoide recept
31 85 7.1 737 2 T14232 NADH2 dehydrogenas
32 84.5 7.0 458 2 T16123 hypothetical prote
33 84 7.0 261 2 T00106 ABC-type transport
34 84 7.0 365 2 C83629 probable permealase
35 84 7.0 442 2 T18917 hypothetical prote
36 83.5 7.0 462 2 E70179 Na+/H+-exchanging
37 83 6.9 247 2 E72865 AcOrf-124 protein
38 83 6.9 409 2 F71828 DNA transfer prote
39 83 6.9 1873 2 A55645 calcium channel, v
40 83 6.9 2139 2 A44677 voltage-dependent
41 83 6.9 2143 2 JH0427 voltage-dependent
42 82.5 6.9 210 2 D89606 protein B0416.3 [i
43 82.5 6.9 276 2 T32689 hypothetical prote
44 82 6.8 157 2 S58002 probable olfactory
45 82 6.8 216 2 F96983 probable membrane

ALIGNMENTS

RESULT 1

G02476

lysosomal-associated multitransmembrane protein - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C/Accession: G02476

R/Lin, B.: Adra, C.N.

Submitted to the EMBL Data Library, March 1996

A/Reference number: H01341

A/Accession: G02476

A/Status: preliminary; translated from GE/EMBL/DBDJ

A/Molecule type: mRNA

A/Residues: 1-262 <LIM>

A/Cross-references: EMBL:U51240; NID:G1255239; PIDN:AAB08975.1; PID:G1255240.

C/Genetics:

A/Gene: LAPTms

Query Match 14.6%; Score 175.5; DB 2; Length 262;

Best Local Similarity 22.8%; Pred. No. 1.3e-08;

Matches 61; Conservative 48; Mismatches 83; Indels 75; Gaps 12;

Qy	14	SCLCCHRTGTLGLVWYLIINAVLLILLALADPDQYNFSSEISGDPFMDANMC	73
Db	11	TCC-CFNVRIATTALAIYHVM-SVLFIEHSVEVAHGKASCKLSQMG----	YLRIADLI 64
Qy	74	IATAISLLMLICMATYGAQKQAAWIIFFCVQIFDPALNMLVAITLIYFNSIQEYI	133
Db	65	SSELLITMLFIISLSLLIGVVKREKYLPLPFLSLQIMDYLLCLLTLLGSYI---	ELPAYL 121
Qy	134	-----RQLPPNFPYR-----DDVMSVNPIC-----	153
Db	122	KLASRASSSKFPLMTLQLDLCISLTLCSSVMEVPTVYLFKSMHMYLPSQEDMPH	181
Qy	154	-----LVLLILFISILTFKGYLISCVWNCYRNGRNS-----SDVLAVYVTSNDTT	201
Db	182	NQFIKMWIISIAFITVLI-FKVTMFKVRCRYLTKOMSVBEKRSKML-----	QK 233
Qy	202	VLPYPYDDATVNGAAKEP-----PPPY 223	
Db	234	VLPYSVEA-LSLPSKTPEGGPAPPY 259	

RESULT 2

T15415

hypothetical protein C05E11.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000

C/Accession: T15415

R/Geisel, C.

Submitted to the EMBL Data Library, April 1996

A/Description: The sequence of C. elegans cosmid C05E11.

A/Reference number: Z18347

A;Residues: 1-301 <WIL>
A;Cross-references: EMBL:Z71186; PIDN:CAA94913.1; GSPDB:GN00028; CESP:F23D12.1
A;Experimental source: clone F23D12
C;Genetics:
A;Gene: CESP:F23D12.1
A;Map position: X
A;Introns: 55/1; 83/2; 109/3; 135/2; 181/3; 211/1; 225/3

	Query Match	7.8%; Score 93.5; DB 2; Length 301;
	Best Local Similarity	22.6%; Pred. No. 0.43;
	Matches	38; Conservative 32; Mismatches 65; Indels 33; Gaps 6;
Qy	14 SCCLCCHVRGCTILLGWYLIINAVLLIIL----	SALADPDQVNFSSSELGGDFEMDD 69
Dd	28 SC--CCHAKTFTIFIGIFEPTICFLIVAVLPDVTTRVCDKLSNDTSESLFDFHEPENI	85
Qy	70 ANMCIAIAI-----SLLMILICAMATYGAYKQRAAWIPFFCYQIFOPALNMLV	118
Dd	86 KNVAVSSFCLNNHIFCFIWAIIQLSVDMVFYGIKTIRFWFFPHIFRICLSLICLV	145
Qy	119 AITVLVPNSIQEVIROLPPNFPVRDDMS-VNPCTVLVILIILPISII	165
Dd	146 DAWLIFRAAS-----GTDDWSVIITP--IVIIAAVAVGY 178	

RESULT 10
S41786
probable sugar transport protein 2 - thermophilic bacterium RT8.B4
N/Alternate names: hypothetical protein 2
C/Species: thermophilic bacterium RT8.B4
C/Date: 07-Sep-1994 #sequence_revision 14-Feb-1997 #text_change 20-Aug-1999
C/Accession: S41786
R/Dwivedi, P.P.; Gibbs, M.D.; Bergquist, P.L.
submitted to the EMBL Data Library, October 1993
A/Description: Cloning, sequencing and over expression of a multifunctional xylanase gene
A/Reference number: S41785
A/Accession: S41786
A/Molecule type: DNA
A/Residues: 1-275 <DWI>
A/Cross-references: EMBL:L18965; NID:g311185; PIDN:AAB42042.1; PID:g311187
C/Superfamily: maltose transport protein malG

Query Match	7.7%	Score 92.5	DB 2	Length 275	
Best local Similarity	22.3%	Pred. No. 0.49			
Matches 53	Conservative	33	Mismatches 69	Indels 83	Gaps 9
Qy	26	ILLGQVYLIINAVVLLIILLSAL	-----ADPQVNFSSSELGGDFEFMDDA	70	
Db	13	IFLAVWTLIADVPFLFMLFSTFKTQSELLSGNTWQIPROPTIGNFSTVLSGNFTYL--K	70		
Qy	71	NMCIAIAISLMLI-ICAMATYGAAYKORAAWIIPFCYQIIPDALN-----MLVA	119		
Db	71	NSVIASVISVVLIIILIISSMAA-----FAPSRKFALNNLLYSIIAGNAIP	116		
Qy	120	ITVLIYP-----NSIQ-----EYIRQLPPNPFYRDDVMSV	149		
Db	117	IHWTLIIIVLTNKKIYDTPVLI GPYVALSI PMSIFILTEFMEPILELEAAKIDGC	176		
Qy	150	NPTCLVLIILIFIS--ILTFKGYLISCWNCYRYINGRNSDVLVYVVTNSDITVLLP	205		
Db	177	SMPELYSDIILLPISAPALIITGVINGYLYNNEFVF-----ALVLTSSPRTPLP	225		

RESULT 11
H87470
AcBr/AcrD/AcrF family protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87470
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A>Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87470
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1032 <STO>
A:Cross-references: GB:AE005673; NID:gl3423218; PIDN:AAK23764.1; GSPDB:GN00148
C:Genetics:
A:Gene: CCI788

	Query Match	7.6%;	Score 91.5;	DB 2;	Length 1032;
	Best Local Similarity	24.4%;	Pred. No. 2.1;		
	Matches	42;	Conservative 21;	Mismatches 72;	Indels 37; Gaps 7;
Qy	59	ELGGDFRFDMDANMCIAITAIISLILMILICAMATYGA YKQRAAWII-----PF	104	:	:
Dd	344	EMGGSIEAGRKANKALAVVFPDLMFLMMVVIFQVRSLSAMVMVLTLAPLALGVAPTLL	903	:	:
Qy	105	FCYQIGFDF-ALNMMLVAITVIYPNSI----QEYIRQLPPNFY----RDDVMSVNPTCLV	155	:	:
Dd	904	IFHQFFGFNAIUGLIALAGAIIMENSILILIQINQEEGLDPFHAVVEATVQRARPVILT	963	:	:
Qy	156	LIIILFISIITFKGYLISCVNN--CYRYINGNRSSDLVYVTSNDTIVLLP	205	:	:
Dd	964	ALA AVFAPIPLT-----LSVFWSMAYNTLIGGTIGTIL-----TLVFLP	1003	:	:

RESULT 12
T14245
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - dermatophytic fungus (Trichophyton
C:Species: mitochondrion Trichophyton rubrum
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T14245
R:de Bievre, C.; Dujon, B.
submitted to the EMBL Data Library, November 1998
A:Description: Organisation of the mitochondrial genome of Trichophyton rubrum, part III
A:Reference number: Z17938
A:Accession: T14245
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-343 <DEB>
A:Cross-references: EMBL:Y18476; PIDN:CAA77189.1
A:Experimental source: isolate IP 1817.89
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC3
A:Note: NADH1
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

RESULT 13
AH1762

```

Db      925  -TAIFTVEILL-KMTTFGAPLHKGA-----FCRNYFNL-LDMLVVGSLV----- 966
QY      135  QLPPNPFYRDDVSNVPTCLVILLIFISILITFKG--YLISCVMNCYRINGRNSSDVL 192
Db      967  ----SFGIOSSAISVVKILRVLRVLRPLRINRAKGLKHVQCFFVAIRTI-----GNIM 1017
QY      193  VYVT 196
Db      1018  IVTT 1021

RESULT 15
JH0422
Voltage-dependent calcium channel complex alpha-1 chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 11-Jan-2000
C;Accession: JH0422; D35901; I60901
R;Hui, A.; Ellinor, P.T.; Krizanova, O.; Wang, J.J.; Diebold, R.J.; Schwartz, A.
Neuron 7, 35-44, 1991
A;Title: Molecular cloning of multiple subtypes of a novel rat brain isoform of
A;Reference number: JH0422; MUID:91299338; PMID:1648940
A;Accession: JH0422
A;Molecule type: mRNA
A;Residues: 1-1646 <HUI>
A;Cross-references: GB:M57682; NID:G206573; PIDN:AAA42015.1; PID:G206574
A;Experimental source: brain
R;Snutch, T.P.; Leonard, J.P.; Gilbert, M.M.; Lester, H.A.; Davidson, N.
Proc Natl. Acad. Sci. U.S.A. 87, 3391-3395, 1990
A;Title: Rat brain expresses a heterogeneous family of calcium channels.
A;Reference number: A35901; MUID:90239020; PMID:1692134
A;Accession: D35901
A;Status: preliminary; nucleic acid sequence not shown; not compared with concen
A;Molecule type: mRNA
A;Residues: 1247-1434 <SNU>
A;Experimental source: brain
R;Yu, A.S.-I.; Hebert, S.C.; Brenner, B.M.; Lytton, J.
Proc. Natl. Acad. Sci. U.S.A. 89, 10494-10498, 1992
A;Title: Molecular characterization and nephron distribution of a family of tra
A;Reference number: A46422; MUID:93066265; PMID:1279681
A;Accession: I60901
A;Status: preliminary; translated from GB/EMBL/DBDB
A;Molecule type: mRNA
A;Residues: 1040-1261,1305-1365 <RES>
A;Cross-references: GB:M99221; NID:G203370; PIDN:AAA40895.1; PID:G203371
A;Experimental source: kidney
C;Comment: Calcium channels are essential for many cellular functions, such as
n.
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: alternative splicing; calcium binding; calcium channel; glycoprotein
F;1463-1491/Domain: calcium binding #status predicted <EPC>
F;154-224,328/Binding site: carbohydrate (Aen) (covalent) #status predicted
F;464,848,1489,1584/Binding site: phosphate (Ser) (covalent) #status predicted
Query Match 7.4%; Score 88.5; DB 2; Length 1646;
Best Local Similarity 25.0%; Pred. No. 6.2;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;
QY      21  VRGTGILLGWYLIINAVVLLILLSALA-----DP-DOYNFSSSELG-GDEFFMDANWCI 74
Db      874  IRVGCCHKLNHHIIFTNLILVFMLSAALAEEDPIRSHSPNTLITGYDYAF----- 925
QY      75  AIAISLLMILICAMATYGAVKORAAWIIPFCYQIFDFALNMLVAITVLIVPNSIQEVIR 134
Db      926  -TAIFTVEILL-KMTTFGAPLHKGA-----FCRNYFNL-LDMLVVGSLV----- 967
QY      135  QLPPNPFYRDDVSNVPTCLVILLIFISILITFKG--YLISCVMNCYRINGRNSSDVL 192
Db      968  ----SFGIOSSAISVVKILRVLRVLRPLRINRAKGLKHVQCFFVAIRTI-----GNIM 1018
QY      193  VYVT 196
Db      1019  IVTT 1022

```

Search completed: February 2, 2004, 14:23:44
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: February 2, 2004, 14:16:30 ; Search time 18 Seconds
(without alignments)
590.446 Million cell updates/sec

Title: US-09-965-529-26

Perfect score: 1200

Sequence: 1 MKVAPWTRFYSNCCCLCH.....YDATVNGAKEPPPPVYSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553.5	45.1	233	1 MTRP_HUMAN	Q15012 homo sapien
2	541.5	45.1	233	1 MTRP_MOUSE	Q60961 mus musculus
3	175.5	14.6	261	1 LAM5_HUMAN	Q13571 homo sapien
4	156	13.0	261	1 LAM5_MOUSE	Q61168 mus musculus
5	95	7.9	1873	1 CCAS_RABIT	P07293 oryctolagus
6	93	7.8	1146	1 CCAS_RAT	Q02485 rattus norv
7	92.5	7.7	275	1 YOR2_CALS	P40980 caldicellul
8	91	7.6	343	1 NULM_TRIRU	Q92238 trichophyto
9	91	7.6	551	1 AAP2_NEUCR	O59942 neurospora
10	89	7.4	297	1 T2R4_MOUSE	Q91kt3 mus musculus
11	88.5	7.4	1610	1 CCAD_MESAU	Q95244 mesocricetu
12	88.5	7.4	2161	1 CCAD_HUMAN	Q01668 homo sapien
13	88.5	7.4	2203	1 CCAD_RAT	P27732 rattus norv
14	88	7.3	274	1 NULM_DROMA	P29867 drosophila
15	87.5	7.3	470	1 MTR_NEUCR	Q13936 homo sapien
16	87	7.2	2221	1 CCAC_HUMAN	P38680 neurospora
17	85.5	7.1	274	1 NULM_DROST	P29868 drosophila
18	85.5	7.1	274	1 NULM_DROST	P29869 drosophila
19	85.5	7.1	667	1 EN70_YEAST	P32802 saccharomyc
20	85	7.1	347	1 CBZ2_MOUSE	P47936 mus musculus
21	83	6.9	247	1 Y124_NFVAC	P41679 autographa
22	83	6.9	1873	1 CCAS_HUMAN	Q13698 homo sapien
23	83	6.9	2139	1 CCAC_MOUSE	Q01815 mus musculus
24	82.5	6.9	210	1 Y743_CAEL	Q11071 caenorhabdi
25	82	6.8	313	1 OIC1_HUMAN	Q15619 homo sapien
26	81.5	6.8	567	1 NULM_HANWI	P48906 hansenula w
27	81	6.8	201	1 PSS_METJA	Q58609 methanococc
28	81	6.8	337	1 OPSX_MOUSE	Q35214 mus musculus
29	81	6.8	341	1 NULM_DROME	P03896 drosophila
30	81	6.8	344	1 NULM_CYACA	P48899 cyanidium c
31	80	6.7	369	1 NULM_ACACA	Q37381 acanthamoeb
32	80	6.7	738	1 NULM_LIGUT	Q5t1a3 ligustrum v
33	80	6.7	2171	1 CCAC_RABIT	P15381 oryctolagus

RESULT 1

ID	MTRP_HUMAN	STANDARD	PRT	233 AA
AC	Q15012			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Lysosomal-associated transmembrane protein 4A (Golgi 4-transmembrane spanning transporter MTP).			
GN	LAPTM4A OR MTRP OR KIAA0108.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=95308325; PubMed=7788527;			
RA	Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S., Tabata S., Ishikawa K.-I., Kawabayashi Y., Kotani H., Nomura N.			
RA	"Prediction of the coding sequences of unidentified human genes. III. The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by analysis of cDNA clones from human cell line KG-1."			
RT	DNA Reel. 2:37-43 (1995).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Muscle;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
CC	-!- FUNCTION: MAY FUNCTION IN THE TRANSPORT OF NUCLEOSIDES AND/OR NUCLEOSIDE DERIVATIVES BETWEEN THE CYTOSOL AND THE LUMEN OF AN INTRACELLULAR MEMBRANE-BOUND COMPARTMENT (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MAY RESIDE IN AN INTRACELLULAR MEMBRANE-BOUND COMPARTMENT (POTENTIAL).			
CC	-!- DOMAIN: THE C-TERMINAL DOMAIN IS NECESSARY FOR RETENTION WITHIN INTRACELLULAR MEMBRANES (BY SIMILARITY).			

Q92cs5 rickettsia
P19397 homo sapien
Q9ack3 mus musculus
P40367 saccharomyc
P39854 staphylococ
P13201 human cytom
P76599 escherichia
Q58086 methanococc
O02100 caenorhabdi
P11442 rattus norv
Q92y49 pseudochiro
Q9xlt9 rattus norv

Query Match 13.0%; Score 156; DB 1; Length 261;
Best Local Similarity 22.4%; Pred. No. 1.2e-06;
Matches 60; Conservative 48; Mismatches 82; Indels 78; Gaps 13;

QY 14 SCCLCCHVTRTGILLGVYLLINAVLLILLISALADPDQYNFSSSELGGDFEFMDANMC 73
DB 11 TCC-CFNIRVATIALAIHVMS-VLLFIEHV-----EVARGKVSCEFPMPLRMA 61
QY 74 IAIASLL---MILICAMATYGVKQRAWIIPFCYQIFDPAFMLVAITVLVYPSIQ 130
DB 62 DLLSFLGLGVLFITISLLGVVKNREKYLIPLSLQIMDFLCLLTLGSIYI---ELP 118
QY 131 EYIRQLPN-FYRDDVMSVN--PTCLVLITLL----- 160
DB 119 AYKLARPRPGSKVPLMTLQLDFCLSLTLCSSYMEVPTLYLNFKNHNNVYLPDSQGV 178
QY 161 ----FISILTF-----KGYLSVCWNCYRYINGRNSDVLVYVTSNDTT----- 201
DB 179 PHSQFINMLIFSAFIVTLVKVYMPKCVVTCYKFLKHNSA-----MEDSSSKMFL 231
QY 202 -VLLPPYDDATVNGAAKEP-----PPPY 223
DB 232 KVALPSYEEA-LSLPPTTPEGDPAPPY 258

RESULT 5
CCAS_RABIT
ID CCAS_RABIT STANDARD; PRT; 1873 AA.
AC P07293;
DT 01-APR-1988 (Rel. 07, Created)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1S subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 3, skeletal muscle).
GN CACNA1S OR CACNA1A3 OR CACNA1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Skeletal muscle;
RX MEDLINE=87258269; PubMed=3073387;
RA Tanabe T., Takeshima H., Mikami A., Flockerzi V., Takahashi H., Kangawa K., Kojima M., Matsuo H., Hirose T., Numa S.;
RT "Primary structure of the receptor for calcium channel blockers from skeletal muscle.";
RL Nature 328:313-318(1987).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=88336904; PubMed=2458626;
RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H., Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A., Schwartz A., Harpold M.M.;
RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2 subunits of a DHP-sensitive calcium channel.";
RL Science 241:1661-1664(1988).
[3]
RN BETA-SUBUNIT BINDING DOMAIN.
RX MEDLINE=94150724; PubMed=7509046;
RA Pragnell M., de Waard M., Mori Y., Tanabe T., Snutch T.P., Campbell K.P.;
RT "Calcium channel beta-subunit binds to a conserved motif in the I-II cytoplasmic linker of the alpha 1-subunit.";
RL Nature 368:67-70(1994).
[4]
RN PHENYLALKYLAMINE-BINDING SITE.
RX MEDLINE=91067656; PubMed=2174553;
RA Striesnig J., Glossmann H., Catterall W.A.;
RT "Identification of a phenylalkylamine binding region within the alpha 1 subunit of skeletal muscle Ca2+ channels.";

Proc. Natl. Acad. Sci. U.S.A. 87:9108-9112(1990).
[5]
RN DIHYDROPYRIDINE-BINDING SITE.
RX MEDLINE=92010109; PubMed=1656465;
RA Nakayama H., Taki M., Striesnig J., Glossmann H., Catterall W.A., Kanaoka Y.;
RT "Identification of 1,4-dihydropyridine binding regions within the alpha 1 subunit of skeletal muscle Ca2+ channels by photoaffinity labeling with diazepam.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:9203-9207(1991).
[6]
RN DIHYDROPYRIDINE-BINDING SITE.
RX MEDLINE=92073369; PubMed=1660150;
RA Striesnig J., Murphy B.J., Catterall W.A.;
RT "Dihydropyridine receptor of L-type Ca2+ channels: identification of binding domains for [3H](+)-PN200-110 and [3H]azidopine within the alpha 1 subunit.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:10769-10773(1991).
[7]
RN PHOSPHORYLATION OF SER-687 AND SER-1617.
RX MEDLINE=89008420; PubMed=2844809;
RA Roehrkasten A., Meyer H.E., Nastainczyk W., Sieber M., Hofmann F.;
RT "CAMP-dependent protein kinase rapidly phosphorylates serine-687 of the skeletal muscle receptor for calcium channel blockers.";
RL J. Biol. Chem. 263:15325-15329(1988).
[8]
RN PHOSPHORYLATION BY CAPK.
RX MEDLINE=89367340; PubMed=2549550;
RA Nunoki K., Florio V., Catterall W.A.;
RT "Activation of purified calcium channels by stoichiometric protein phosphorylation.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:6816-6820(1989).
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1S GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), AND BY OMEGA-AGATOXIN-III (OMEGA-AGA-III). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTAINING THE ALPHA-1S SUBUNIT PLAY AN IMPORTANT ROLE IN EXCITATION-CONTRACTION COUPLING IN SKELETAL MUSCLE.
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY. AN ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE CHANNEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE SPECIFIC.
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- DOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE RYANODINE RECEPTOR, AND IS THEREFORE IMPORTANT FOR CALCIUM RELEASE FROM THE ENDOPLASMIC RETICULUM NECESSARY FOR MUSCLE CONTRACTION.
CC -1- PTM: THE ALPHA-1S SUBUNIT IS FOUND IN TWO ISOFORMS IN THE SKELETAL MUSCLE: A MINOR FORM OF 212 KDA CONTAINING THE COMPLETE AMINO ACID SEQUENCE, AND A MAJOR FORM OF 190 KDA DERIVED FROM THE FULL-LENGTH FORM BY POST-TRANSLATIONAL PROTEOLYSIS CLOSE TO PHE-1690.
CC -1- PTM: BOTH THE MINOR AND MAJOR FORMS ARE PHOSPHORYLATED IN VITRO BY CAPK. PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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EMBL; X05921; CRA29355.1; -;
EMBL; M23919; AAA31159.1; -;
PIR; A30063; A30063.
PDB; 1DU1; 19-JUL-00.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002077; Ca_channel.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005446; LVDCALphal.
DR InterPro; IPR005450; LVDCALphals.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; ion_trans_4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR01630; LVDCALPHAL.
DR PRINTS; PR01634; LVDCALPHALS.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Repeat; Multigene family;
KW Calcium-binding; Phosphorylation; Polymorphism; 3D-structure.
FT REPEAT 38 337 I.
FT REPEAT 418 664 II.
FT REPEAT 786 1068 III.
FT REPEAT 1105 1384 IV.
FT DOMAIN 1 51
FT TRANSMEM 52 70
FT DOMAIN 71 88
FT TRANSMEM 89 108
FT DOMAIN 109 120
FT TRANSMEM 121 139
FT DOMAIN 140 160
FT TRANSMEM 161 179
FT DOMAIN 180 198
FT TRANSMEM 199 218
FT DOMAIN 219 309
FT TRANSMEM 310 334
FT DOMAIN 335 432
FT TRANSMEM 433 451
FT DOMAIN 452 466
FT TRANSMEM 467 486
FT DOMAIN 487 494
FT TRANSMEM 495 513
FT DOMAIN 514 523
FT TRANSMEM 524 542
FT DOMAIN 543 561
FT TRANSMEM 562 581
FT DOMAIN 582 636
FT TRANSMEM 637 661
FT DOMAIN 662 799
FT TRANSMEM 800 818
FT DOMAIN 819 834
FT TRANSMEM 835 854
FT DOMAIN 855 866
FT TRANSMEM 867 885
FT DOMAIN 886 892
FT TRANSMEM 893 911
FT DOMAIN 912 930
FT TRANSMEM 931 950
FT DOMAIN 951 1040
FT TRANSMEM 1041 1065
FT DOMAIN 1066 1118
FT TRANSMEM 1119 1137
FT DOMAIN 1138 1152
FT TRANSMEM 1153 1172
FT DOMAIN 1173 1180
FT TRANSMEM 1181 1199
S1 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S6 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S6 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT III (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT III (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT III (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S6 OF REPEAT III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT IV (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT IV (POTENTIAL).

FT DOMAIN 1200 1231 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1232 1250 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1251 1269 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1270 1289 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1290 1356 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1357 1381 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1382 1873 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 357 374 BINDING TO THE BETA SUBUNIT.
FT DOMAIN 562 568 POLY-LEU.

Query Match 7.9%; Score 95; DB 1; Length 1873;
Best Local Similarity 24.0%; Pred. No. 1.8;
Matches 46; Conservative 31; Mismatches 69; Indels 46; Gaps 9;

Qy 12 SNSCCLCHVTRGTGILLGVYLIINAVVLLILLGALA----DPQYNFSSSELGDDPEFM 67
Db 785 TNKRVVLCH----RIVNATWF--TNFILLFILLSAALAEEDPIRAESVRNQLIGYFD-- 836
Qy 68 DDANMCIAIAISLMLILICAMATYAYKQRAAWIIPFCVQIFDPALNMLVAITVLIYPN 127
Db 837 -----IAFTSVFTVEIVLKMVTYGAFLHKS-----FCRNYFNI-LDLLVAVVSLI--- 881
Qy 128 SIQYIRQLPFPNFPYRDVMSVNTCLVLLILLFISILIFKG--YLISCWNCVRYING 185
Db 882 -----SMGLSSTISVVKILRVLRVLRPRINRAKGLKHVVQCVFVAIRTGN 930
Qy 186 RNSSDVLVYVTS 197
Db 931 -----IVLVT 936

RESULT 6
CCAS RAT STANDARD; PRT; 1146 AA.
ID CCAS RAT STANDARD; PRT; 1146 AA.
AC Q02485; P70484; Q01553; Q62817;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1s subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 3, skeletal muscle) (ROB1) (Fragment).
DE GN CACNA1S OR CACNA1A3 OR CACN1 OR CACN1 OR CCHLIA3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93122775; PubMed=1335956;
RA Chin H., Krall M., Kim H.-L., Kozak C.A., Mock B.A.;
RT "The gene for the alpha-1 subunit of the skeletal muscle dihydropyridine-sensitive calcium channel (Cchla3) maps to mouse chromosome 1.";
RL Genomics 14:1089-1091 (1992).
RN [2]
RP SEQUENCE OF 597-691 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=9306265; PubMed=1279681;
RA Yu A.S.-L., Hebert S.C., Brenner B.M., Lyttton J.;
RT "Molecular characterization and nephron distribution of a family of transcripts encoding the pore-forming subunit of Ca2+ channels in the kidney.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498 (1992).
RN [3]
RP SEQUENCE OF 359-658 FROM N.A. (ISOFORM ROB1).
RC TISSUE=Osteosarcoma;
RX MEDLINE=96074617; PubMed=7479909;
RA Barry E.L.R., Geesek F.A., Froehner S.C., Friedman P.A.;
RT "Multiple calcium channel transcripts in rat osteosarcoma cells: selective activation of alpha 1D isoform by parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918 (1995).
RN [4]
RP PHOSPHORYLATION BY CAPK.

RX MEDLINE=91065881; PubMed=2174428;
 RA Lai Y., Seagar M.J., Takahashi M., Catterall W.A.;
 RT "Cyclic AMP-dependent phosphorylation of two size forms of alpha 1
 subunits of L-type calcium channels in rat skeletal muscle cells.";
 RL J. Biol. Chem. 265:20839-20848(1990).
 CC -|- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
 ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1S
 GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
 CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
 GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),
 PHENYLALKYLAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-III
 (OMEGA-AGA-III). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
 GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
 CALCIUM CHANNELS CONTAINING THE ALPHA-1S SUBUNIT PLAY AN IMPORTANT
 ROLE IN EXCITATION-CONTRACTION COUPLING IN SKELETAL MUSCLE.
 CC -|- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
 COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
 FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY. AN
 ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE
 CHANNEL.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=002485-1; Sequence=Displayed;
 CC Name=ROB1;
 CC IsoId=002485-2; Sequence=VSP 000939;
 CC -|- TISSUE SPECIFICITY: SKELETAL MUSCLE SPECIFIC.
 CC -|- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -|- DOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE
 RYANODINE RECEPTOR, AND IS THEREFORE IMPORTANT FOR CALCIUM RELEASE
 FROM THE ENDOPLASMIC RETICULUM NECESSARY FOR MUSCLE CONTRACTION.
 CC -|- PTM: PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL
 FUNCTION (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L04684; AAA40844.1; -;
 DR EMBL; M99220; AAA40894.1; -;
 DR EMBL; U31816; AAA89158.1; -;
 DR PIR; A46422; A46422.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_chan.
 DR InterPro; IPR005820; M-channel_nlg.
 DR Pfam; PF00520; Ion_chan; 2.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Alternative splicing.
 FT NON TER 1 1
 FT REPEAT 73 355 III.
 FT REPEAT 392 671 IV.
 FT DOMAIN <1 86 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 87 105 S1 OF REPEAT III (POTENTIAL).

FT DOMAIN 106 121 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 122 141 S2 OF REPEAT III (POTENTIAL).
 FT DOMAIN 142 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 154 172 S3 OF REPEAT III (POTENTIAL).
 FT DOMAIN 173 179 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 180 198 S4 OF REPEAT III (POTENTIAL).
 FT DOMAIN 199 217 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 218 237 S5 OF REPEAT III (POTENTIAL).
 FT DOMAIN 238 327 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 328 352 S6 OF REPEAT III (POTENTIAL).
 FT DOMAIN 353 405 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 406 424 S1 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 425 439 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 440 459 S2 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 460 467 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 468 485 S3 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 487 518 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 519 537 S4 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 538 556 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 557 576 S5 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 577 643 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 644 668 S6 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 669 1146 CYTOPLASMIC (POTENTIAL).
 FT SITE 301 301 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT SITE 610 610 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
 FT BINDING 275 364 DIHYDROPYRIDINES (BY SIMILARITY).
 FT BINDING 624 690 DIHYDROPYRIDINES (BY SIMILARITY).
 FT BINDING 636 679 PHENYLALKYLAMINES (BY SIMILARITY).
 FT MOD_RES 679 679 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT CA_BIND 697 708 BY SIMILARITY.
 FT CARBOHYD 428 428 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPIC 491 509 Missing (in isoform ROB1).
 FT CONFLICT 548 548 /FTId=VSP_000939.
 FT CONFLICT 610 610 I -> T (IN REF. 3).
 FT CONFLICT 610 610 E -> A (IN REF. 3).
 SQ SEQUENCE 1146 AA; 130143 MW; 4BBE944261BE1A95 CRC64;
 Query Match 7.8%; Score 93; DB 1; Length 1146;
 Best Local Similarity 23.4%; Pred. No. 1.6;
 Matches 45; Conservative 33; Mismatches 68; Indels 46; Gaps 9;
 QY 12 SNSCCLCHVTRGTGTLIGVWYLIINAVLLILLSALA----DPDQVNFSSSELGGDFEPM 67
 Db 72 TNKIRVLCH---RIVNATWF--TNFILLILLSAALAAEDPIRADSMENQILEYFDYV 125
 QY 68 DDANMCIAISLMLILICAMATYGYKQRAAWIIPFCYQIFDFALNMLVAITVLIYPN 127
 Db 126 FTAFTVEIVLK-----MTTYGAPLHKGS-----FCRNYFNI-LDLLEWAVSLI--- 168
 QY 128 SIOEYIRQLPNFPYRDDVMSVNPVTCVLVLLIPISILITFKG--YLISCVWNCYRYING 185
 Db 169 -----SMGLESSAISVVKILRVLRLPLRAINRAKGLKHVQVCVFAIRTIGN 217
 QY 186 RNSGSDVLVYVTS 197
 Db 218 -----IVLVTT 223
 RESULT 7
 YOR2_CALSR
 ID_YOR2_CALSR STANDARD; PRT; 275 AA.
 AC P40980;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical 30.9 kDa protein in xylR 5' region (ORF2).
 OS Caldicellulosiruptor sp. (strain R-8B.4).
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
 OC Caldicellulosiruptor.
 OK NCBI_TaxID=28238;
 RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=97077616; PubMed=8920183;
RA Dwivedi P.P., Gibbs M.D., Saul D.J., Bergquist P.L.;
RT "Cloning, sequencing and overexpression in Escherichia coli of a
RT xylanase gene, xynA from the thermophilic bacterium RT8B.4 genus
RT Caldicellulosiruptor";
RL Appl. Microbiol. Biotechnol. 45:86-93(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY. MALFG SUBFAMILY.
CC
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CC
DR EMBL; L18965; AAB42042.1; -;
DR PIR; S41786; S41786.
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD transp. 1.
DR PROSITE; PS00402; BPD_TRANS_PNN_MEMBER; 1.
KW Hypothetical protein; Transmembrane; Transport.
FT TRANSMEM 11 31
FT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 108 128 POTENTIAL.
FT TRANSMEM 136 156 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 239 259 POTENTIAL.
SQ SEQUENCE 275 AA; 30857 MW; BD7A3246B4F50199 CRC64;

Query Match 7.7%; Score 92.5; DB 1; Length 275;
Best Local Similarity 22.3%; Pred. No. 0.44; Indels 83; Gaps 9;
Matches 53; Conservative 33; Mismatches 69;

Qy 26 ILLGVYLIINAVVLLILLAL-----ADPQVNFSSSELGGDFEFMDA 70
Db 13 IFLAVTLLIADVPLFMLEFTSFKQSELSSGNTWQIPQPTIGNEFTVLEGNFTYL--K 70

Qy 71 NWCIAISLLMIL-ICAMATYKAYKORAAWIIPFCYQIDFALN-----MLVA 119
Db 71 NSVIAVSIVVLLIISSMAA-----FAPSRKFALNNLLYSIIAGMAIP 116

Qy 120 ITVLIYP-----NSTQ-----EYIROLPPNPPYRDDVMSV 149
Db 117 IHVLIPIYVITNKIKLYDTVFALIGPVVALSLPMSIFILTFKREIPLLEEAAKIDGC 176

Qy 150 NPTCLVLIILLFIS--IILTFKGYLSCVWNCYRYINGRNSSDVLVYVTSNDTTVLLP 205
Db 177 SMERLYSDILLPLSAPALITVGYNGTYLWNEFVF-----ALVITSPTRTTLP 225

RESULT 8
NUIUM TRIRU STANDARD; PRT; 343 AA.
AC Q92238;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 1 [EC 1.6.5.3].
GN ND1 OR NADH1.
OS Trichophyton rubrum.
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Oxygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
OC Trichophyton.
OX NCBI_TaxID=5551;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 1817.89;
RX MEDLINE=99146870; PubMed=10022946;

de Bievre C., Dujon B.;
"Organisation of the mitochondrial genome of Trichophyton rubrum III.
DNA sequence analysis of the NADH dehydrogenase subunits 1, 2, 3, 4,
5 and the cytochrome b gene.";
Curr. Genet. 35:30-35(1999).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
CC
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CC
DR EMBL; Y18476; CAA77189.1; -;
DR PIR; T14245; T14245.
DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 343 AA; 38239 MW; D29CD3BF97CFED64 CRC64;

Query Match 7.6%; Score 91; DB 1; Length 343;
Best Local Similarity 21.7%; Pred. No. 0.74; Indels 58; Gaps 12;
Matches 47; Conservative 45; Mismatches 67;

Qy 9 RFVNSCCLCHVTRTGILG-----VWYLI-INAVVLLILLALADPDQVNFSSSE 59
Db 153 RFY-----ILLVILFTGSLNLTTFIESQKVYFLLPLFLIFPIFGICTAETNRAPFDLAE 208

Qy 60 LGGDF--EFWDDANWCIAIALSL-----MLICAMAT---YGAYKORAAWIIPFCYQI 109
Db 209 AESVLSVGFMTESAVIFMIFFFLAQYASIVLICILSSVLFGLGYLN---ILPLNTYV 264

Qy 110 FDF-----ALNMLVAITVLIYPSIOEYIRQLPPNPPYRDDVMSVNPCTCLVL 156
Db 265 CDFNSLFSVLYINGLSLNLAKTAFLIF---VFIWVASFPPIRF-DQLMSVCVMTLLP 320

Qy 157 IILLFISIIITFKGYLSCVWNCYRYINGRNSDVLV 193
Db 321 IIIAYV-----VLLPCI-----VIGLNSILLI 343

RESULT 9
AAP2_NEUCR
ID AAP2_NEUCR STANDARD; PRT; 551 AA.
AC O59942;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Amino acid permease 2.
GN AAP-2 OR AAP2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RL Margolles-Clark E., Bowman B.J.;
Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: Belongs to the amino acid permease family.
CC
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CC

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CC EMBL; AF053231; AAC08355.1;
DR InterPro; IPR002293; AA/rel_permease.1;
DR InterPro; IPR004756; AA_permease.
DR InterPro; IPR004840; AAC_permease.
DR InterPro; IPR004841; Permease.
DR PFAM; PF00324; aa_permeases; 1.
DR TIGRFAMs; TIGR00907; 2A0304; 1.
DR PROSITE; PS00218; AMINO ACID PERMEASE 1; 1.
KW Transport; Amino-acid transport; Transmembrane.
FT TRANSMEM 66 86 POTENTIAL.
FT TRANSMEM 90 110 POTENTIAL.
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 188 208 POTENTIAL.
FT TRANSMEM 214 234 POTENTIAL.
FT TRANSMEM 255 275 POTENTIAL.
FT TRANSMEM 301 321 POTENTIAL.
FT TRANSMEM 347 367 POTENTIAL.
FT TRANSMEM 399 419 POTENTIAL.
FT TRANSMEM 424 444 POTENTIAL.
FT TRANSMEM 464 484 POTENTIAL.
FT TRANSMEM 496 516 POTENTIAL.
SQ SEQUENCE 551 AA; 59869 MW; C812C646B82F9ADF CRC64;

Query Match 7.6%; Score 91; DB 1; Length 551;
Best Local Similarity 22.0%; Pred. No. 1.2;
Matches 37; Conservative 32; Mismatches 53; Indels 46; Gaps 9;

Qy 22 RTGTILLGVW-YLINAVALVLLISALADPPQYNFSSSELGGDFEFDANWC-IAIAIS 79
Db 395 RSQTPLIAVTVYAVLEIIINLGLA-----SSTAIGAVF-----NVCTVALNVS 438
Qy 80 LLMILICAMATYGVAKQKAAWIIFFCQVIFDFALNMLVAITLVLYPNSIQEYIRQLPPN 139
Db 439 YVPIPLICKK-VYGR-MQKGPWHMGKYSVWNAFVAVNTFWAVIFF----- 482
Qy 140 FPYRDDVMSVNPCTCLVILILIFISILTFKGYLISCVNVCYRYINGRN 187
Db 483 FPTRVPTPENVAIVVFFVLLALVF-----W-----YTHGRH 518

RESULT 10
ID T2R4 MOUSE STANDARD; PRT; 297 AA.
AC Q9JKT3.
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Taste receptor type 2 member 4 (T2R4) (Taste receptor type 2 member
8) (T2R8).
GN TAS2R4 OR TAS2R8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TOPOLOGY.
RC STRAIN=129/SWJ;
RX MEDLINE=20222571; PubMed=10761934;
RA Adler E., Hoon M.A., Mueller K.L., Chandrashekar J., Ryba N.J.P.,
RA Zuker C.S., Ryba N.J.;
RT "A novel family of mammalian taste receptors.";
RL Cell 100:693-702(2000).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=20222572; PubMed=10761935;
RA Chandrashekar J., Mueller K.L., Hoon M.A., Adler E., Feng L., Guo W.,
RA Zuker C.S., Ryba N.J.;
RT "T2R8 function as bitter taste receptors.";
RL Cell 100:703-711(2000).
RN [3]
RP REVIEW.
RX MEDLINE=22135574; PubMed=12139982;

RA Montmayeur J.-P., Matsunami H.;
RT "Receptors for bitter and sweet taste.";
RL Curr. Opin. Neurobiol. 12:366-371(2002).
RN [4]
RP REVIEW.
RX MEDLINE=21634924; PubMed=11696554;
RA Margolske R.F.;
RT "Molecular mechanisms of bitter and sweet taste transduction.";
RL J. Biol. Chem. 277:1-4(2002).
RN [5]
RP REVIEW.
RX MEDLINE=22469025; PubMed=12581520;
RA Zhang Y., Hoon M.A., Chandrashekar J., Mueller K.L., Cook B., Wu D.,
RA Zuker C.S., Ryba N.J.;
RT "Coding of sweet, bitter, and umami tastes: different receptor cells
sharing similar signaling pathways.";
RL Cell 112:293-301(2003).
CC -1- FUNCTION: Receptor that may play a role in the perception of
bitterness and is gustducin-linked. Activated by denatonium and
6-n-propyl-2-thiouracil. May play a role in sensing the chemical
composition of the gastrointestinal content. The activity of this
receptor may stimulate alpha gustducin, mediate PLC-beta-2
activation and lead to the gating of TRPM5.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells
of the tongue and palate epithelium and exclusively in gustducin-
positive cells. Expressed in 15% taste bud cells in circumvallate
and foliate papillae but only in 2% in fungiform papillae.
CC -1- MISCELLANEOUS: Most taste cells may be activated by a limited
number of bitter compounds; individual taste cells can
discriminate among bitter stimuli.
CC -1- SIMILARITY: Belongs to family T2R of G-protein coupled receptors.
CC -1- CAUTION: This protein was previously referred to T2R8, but due to
its high similarity towards the human T2R4 sequence it is
considered to be T2R4.

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EMBL; AF227148; AAF43921.1;
Pfam; PF05296; TAS2R; 1
Receptor; G-protein coupled receptor; Transmembrane.
DOMAIN 1 11 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 12 32 1 (POTENTIAL).
FT DOMAIN 33 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 47 67 2 (POTENTIAL).
FT DOMAIN 68 80 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 81 101 3 (POTENTIAL).
FT DOMAIN 102 128 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 129 149 4 (POTENTIAL).
FT DOMAIN 150 171 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 172 192 5 (POTENTIAL).
FT DOMAIN 193 229 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 230 250 6 (POTENTIAL).
FT DOMAIN 251 260 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 261 281 7 (POTENTIAL).
FT DOMAIN 282 297 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 297 AA; 34202 MW; EC2C1EA806571F80 CRC64;

Query Match 7.4%; Score 89; DB 1; Length 297;
Best Local Similarity 24.7%; Pred. No. 0.96;
Matches 48; Conservative 30; Mismatches 76; Indels 40; Gaps 9;

Qy 21 VRTGTYLLGVWYLIINAVVLLILLISA-----LADPPQYNFSSSELGGDFEFDANWC 74
Db 9 VFAASVFLNFGVIANLFIIVIIKTNWSRRIASPRILFS-----L 51
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FT TRANSMEM 1126 1146 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1147 1203 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1204 1222 S1 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1223 1237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1238 1257 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1258 1264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1265 1286 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1287 1311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1312 1331 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1332 1350 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1351 1370 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1371 1437 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1438 1462 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1463 1610 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1 6 POLY-MET.
FT DOMAIN 652 658 POLY-LEU.
FT TRANSMEM 826 836 POLY-GLU.
FT DOMAIN 428 445 BINDING TO THE BETA SUBUNIT
FT SITE 363 363 (BY SIMILARITY).
FT SITE 704 704 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT SITE 1099 1099 (BY SIMILARITY).
FT SITE 1404 1404 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT SITE 1099 1099 (BY SIMILARITY).
FT SITE 1404 1404 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT BINDING 1073 1163 DIHYDROPYRIDINES (BY SIMILARITY).
FT BINDING 1418 1484 DIHYDROPYRIDINES (BY SIMILARITY).
FT BINDING 1430 1473 PHENYLALKYLAMINES (BY SIMILARITY).
FT MOD RES 1473 1473 PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT CA BIND 1491 1502 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 328 328 GFSDAMTFDSLVIGSIIDVASEADPTSESLPPTAT
FT VARSPLIC 1261 1303 PG -> HYFTDAMTFDALIVGVSVDAITEVN (in
FT FT isoform CACH3D).
FT FT /FTId=VSP 000915.
SQ SEQUENCE 1610 AA; 182327 MW; B3B2E3794D936F79 CRC64;

Query Match 7.4%; Score 88.5; DB 1; Length 1610;
Best Local Similarity 25.0%; Pred. No. 5.7;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy 21 VRTGILLGVWYLIINAVVLLILSALA----DP-DQVNSSSELG-GDFEFMDANMCI 74
Db 873 IRVGHKLNHIPTNLILVFMILSSAALAEEDPIRSHSPFTNLIGYFDYAF----- 924

Qy 75 AIAISLLMILICAMATYQKRAAIIIPFCYQIFQFALNMLVAITVLIYPSIQBYIR 134
Db 925 -TAIFTVEILL-KMTTFGAPLHKG-----FCRYFNIL-LDMLVGVSLV----- 966

Qy 135 QLPNFPYRDVMSVNPCLVLIILLFTSILITPKG--YLISCWNCVRYINGRSSDVL 192
Db 967 ----SFGIQSSAISVKILRLVRLPLRAINRAKGLKHVVQCQVFAIRTI-----GNIM 1017

Qy 193 VYVT 196
Db 1018 IVTT 1021

RESULT 12
CCAD_HUMAN
ID CCAD_HUMAN STANDARD; PRT; 2161 AA.
AC Q01668; Q13916; Q13931;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium
GN channel, L type, alpha-1 polypeptide, isoform 2).
OS Homo sapiens (Human).
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OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM NEURONAL-TYPE).
RC TISSUE=Neuroblastoma;
RX MEDLINE=92110010; PubMed=1309651;
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R., Velicelebi G.,
RA Ellis S.B., Harpold M.M.;
RT "Structure and functional expression of alpha 1, alpha 2, and beta
RL subunits of a novel human neuronal calcium channel subtype.";
RN Neuron 8:71-84(1992).
RP [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA-CELL-TYPE).
RC TISSUE=Pancreatic islets;
RX MEDLINE=92115705; PubMed=1309948;
RA Seino S., Chen L., Seino M., Blondel O., Takeda J., Johnson J.H.,
RA Bell G.I.;
RT "Cloning of the alpha 1 subunit of a voltage-dependent calcium
RL channel expressed in pancreatic beta cells.";
RN Proc. Natl. Acad. Sci. U.S.A. 89:584-588(1992).
RP [3]
RP SEQUENCE FROM N.A. (ISOFORM BETA-CELL-TYPE), AND VARIANT NIDDM.
RX MEDLINE=96044438; PubMed=7557998;
RA Yamada Y., Masuda K., Li Q., Ihara Y., Kubota A., Miura T.,
RA Nakamura K., Fujii Y., Seino S., Seino Y.;
RT "The structures of the human calcium channel alpha 1 subunit
RL (CACNL1A2) and beta subunit (CACNLB3) genes.";
CC Genomics 27:312-319(1995).
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D
CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),
CC PHENYLALKYLAMINES, BENZOTHAZEPINES, AND BY OMEGA-ACETOXIN-IIIA
CC (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
CC GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=Neuronal-type;
CC IsoId=Q01668-1; Sequence=Displayed;
CC Name=Beta-cell-type;
CC IsoId=Q01668-2; Sequence=VSP_000914;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN PANCREATIC ISLETS AND IN BRAIN,
CC WHERE IT HAS BEEN SEEN IN HIPPOCAMPUS, BASAL GANGLIA, HABENULA AND
CC THALAMUS. NO EXPRESSION IN SKELETAL MUSCLE.
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- POLYMORPHISM: A CHANGE FROM SEVEN TO EIGHT ATG TRINUCLEOTIDE
CC REPEATS, RESULTING IN AN ADDITIONAL N-TERMINAL METHIONINE, HAS
CC BEEN FOUND IN A PATIENT WITH NON-INSULIN-DEPENDENT DIABETES
CC MELLITUS (NIDDM).
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
CC -----
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DR EMBL; M76558; AAA58402.1; -
DR EMBL; M83566; AAA35629.1; -
DR EMBL; D43747; BAA07804.1; -
DR EMBL; D43705; BAA07804.1; JOINED.
DR EMBL; D43706; BAA07804.1; JOINED.
DR EMBL; D43707; BAA07804.1; JOINED.
DR EMBL; D43708; BAA07804.1; JOINED.
DR EMBL; D43709; BAA07804.1; JOINED.
DR EMBL; D43710; BAA07804.1; JOINED.
DR EMBL; D43711; BAA07804.1; JOINED.
DR EMBL; D43712; BAA07804.1; JOINED.
DR EMBL; D43713; BAA07804.1; JOINED.
DR EMBL; D43714; BAA07804.1; JOINED.
DR EMBL; D43715; BAA07804.1; JOINED.
DR EMBL; D43716; BAA07804.1; JOINED.
DR EMBL; D43717; BAA07804.1; JOINED.
DR EMBL; D43718; BAA07804.1; JOINED.
DR EMBL; D43719; BAA07804.1; JOINED.
DR EMBL; D43720; BAA07804.1; JOINED.
DR EMBL; D43721; BAA07804.1; JOINED.
DR EMBL; D43722; BAA07804.1; JOINED.
DR EMBL; D43723; BAA07804.1; JOINED.
DR EMBL; D43724; BAA07804.1; JOINED.
DR EMBL; D43725; BAA07804.1; JOINED.
DR EMBL; D43726; BAA07804.1; JOINED.
DR EMBL; D43727; BAA07804.1; JOINED.
DR EMBL; D43728; BAA07804.1; JOINED.
DR EMBL; D43729; BAA07804.1; JOINED.
DR EMBL; D43730; BAA07804.1; JOINED.
DR EMBL; D43731; BAA07804.1; JOINED.
DR EMBL; D43732; BAA07804.1; JOINED.
DR EMBL; D43733; BAA07804.1; JOINED.
DR EMBL; D43734; BAA07804.1; JOINED.
DR EMBL; D43735; BAA07804.1; JOINED.
DR EMBL; D43736; BAA07804.1; JOINED.
DR EMBL; D43737; BAA07804.1; JOINED.
DR EMBL; D43738; BAA07804.1; JOINED.
DR EMBL; D43739; BAA07804.1; JOINED.
DR EMBL; D43740; BAA07804.1; JOINED.
DR EMBL; D43741; BAA07804.1; JOINED.
DR EMBL; D43742; BAA07804.1; JOINED.
DR EMBL; D43743; BAA07804.1; JOINED.
DR EMBL; D43744; BAA07804.1; JOINED.
DR EMBL; D43745; BAA07804.1; JOINED.
DR EMBL; D43746; BAA07804.1; JOINED.
DR EMBL; HGNC:1391; CACNAID.
DR MIM; 114206; -
DR GO; GO:0005891; C: voltage-gated calcium channel complex; TAS.
DR GO; GO:0015270; F: dihydropyridine-sensitive calcium channel a.; TAS.
DR GO; GO:0006832; P: small molecule transport; TAS.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002077; Ca channel.
DR InterPro; IPR002111; Ca channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR005446; LVDCALphal.
DR InterPro; IPR005452; LVDCALphalD.
DR InterPro; IPR005920; M+channel_nlg.
DR Pfam; PF00520; Ion trans. 4.
DR PRINTS; PR00167; CCHANNEL.
DR PRINTS; PR01630; LVDCALPHAL.
DR PRINTS; PR01636; LVDCALPHALD.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Repeat; Multigene family;
KW Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;
KW Triplet repeat expansion.
FT REPEAT 113 409 I.
FT REPEAT 509 755 II.
FT REPEAT 873 1155 III.

FT REPEAT 1192 1467
FT DOMAIN 1 126
FT TRANSMEM 127 145
FT DOMAIN 146 163
FT TRANSMEM 164 183
FT DOMAIN 184 195
FT TRANSMEM 196 214
FT DOMAIN 215 235
FT TRANSMEM 236 254
FT DOMAIN 255 273
FT TRANSMEM 274 293
FT DOMAIN 294 381
FT TRANSMEM 382 406
FT DOMAIN 407 523
FT TRANSMEM 524 543
FT DOMAIN 544 558
FT TRANSMEM 559 577
FT DOMAIN 578 585
FT TRANSMEM 586 604
FT DOMAIN 605 614
FT TRANSMEM 615 633
FT DOMAIN 634 652
FT TRANSMEM 653 673
FT DOMAIN 674 727
FT TRANSMEM 728 752
FT DOMAIN 753 886
FT TRANSMEM 887 905
FT DOMAIN 906 921
FT TRANSMEM 922 941
FT DOMAIN 942 953
FT TRANSMEM 954 972
FT DOMAIN 973 978
FT TRANSMEM 979 998
FT DOMAIN 999 1017
FT TRANSMEM 1018 1037
FT DOMAIN 1038 1127
FT TRANSMEM 1128 1148
FT DOMAIN 1149 1205
FT TRANSMEM 1206 1224
FT DOMAIN 1225 1239
FT TRANSMEM 1240 1259
FT DOMAIN 1260 1266
FT TRANSMEM 1267 1288
FT DOMAIN 1289 1313
FT TRANSMEM 1314 1333

Query Match 7.4%; Score 88.5; DB 1; Length 2161;
Best Local Similarity 25.0%; Pred. No. 7.6;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy 21 VRTGTLILGVYLLINAVLLILLSALA---DP-DYVNFSSSELG-GDREFMDANNCI 74
Db 875 IRVCHKLINHIPTNLILFIMUSSAALAEADPIRSHSFNTLIGFDYAF----- 926
Qy 75 AIAISLMLICAMATYGAYKQRAWIIPFCYQIFDFAIMLVAVITVLIYPSIQEYIR 134
Db 927 -TAFTVEILL-KMTTFGAFHLKGA----FCRNVENI-LDMLVGVSLV----- 968
Qy 135 QLPNFPYRDDVMVNPTCLVLIILFISILTPKG--YLISCWNCVRYINGRNSDVL 192
Db 969 ----SFGIQSSAISVWKILRVLRPLRAINRAKGLKHVVQCVFAIRTI-----GNIM 1019
Qy 193 VYVT 196
Db 1020 IVTT 1023

RESULT 13
CCAD RAT
ID -CCAD RAT STANDARD; PRT: 2203 AA.
AC P27732; O09022; O09023; Q01542; Q62691; Q62815; Q63491;
AC Q63492;
DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium
DE channel, L type, alpha-1 polypeptide, isoform 2) (Rat brain class D)
DE (RBD)
GN CACNA1D OR CACNA1A2 OR CCHL1A2 OR CACH3 OR CACNA4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Insulinoma;
RX MEDLINE=95280950; PubMed=7760845;
RA Ihara Y., Yamada Y., Fujii Y., Gono T., Yano H., Yasuda K.,
RA Inagaki N., Seino Y., Seino S.;
RT "Molecular diversity and functional characterization of voltage-
RT dependent calcium channels (CACNA4) expressed in pancreatic beta-
RT cells.";
RL Mol. Endocrinol. 9:121-130(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 3; 6; 7; 8 AND 14).
RC TISSUE=Brain;
RX MEDLINE=9129338; PubMed=1648940;
RA Hui A., Ellinger P.T., Krikanova O., Wang J.-J., Diebold R.J.,
RA Schwartz A.;
RT "Molecular cloning of multiple subtypes of a novel rat brain isoform
RT of the alpha-1 subunit of the voltage-dependent calcium channel.";
RL Neuron 7:35-44(1991).
RN [3]
RP SEQUENCE OF 1-125 FROM N.A.
RX MEDLINE=96040125; PubMed=7553731;
RA Kamp T.J., Mitas M., Fields K.L., Asch S., Chin H., Marban E.,
RA Nirenberg M.;
RT "Transcriptional regulation of the neuronal L-type calcium channel
RT alpha 1D subunit gene.";
RL Cell. Mol. Neurobiol. 15:307-326(1995).
RN [4]
RP SEQUENCE OF 1100-1410 FROM N.A. (ISOFORMS 11 AND 12).
RC TISSUE=Kidney;
RX MEDLINE=93066265; PubMed=1279681;
RA Yu A.S.L., Hebert S.C., Brenner B.M., Lytton J.;
RT "Molecular characterization and nephron distribution of a family of
RT transcripts encoding the pore-forming subunit of Ca²⁺ channels in the
RT kidney.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498(1992).
RN [5]
RP SEQUENCE OF 1218-1498 FROM N.A. (ISOFORM 13).
RC TISSUE=Osteosarcoma;
RX MEDLINE=96074617; PubMed=7479909;
RA Barry E.L.R., Gesek F.A., Froehner S.C., Friedman P.A.;
RT "Multiple calcium channel transcripts in rat osteosarcoma cells:
RT selective activation of alpha 1D isoform by parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918(1995).
RN [6]
RP SEQUENCE OF 1200-1493 FROM N.A. (ISOFORMS 3; 4; 5; 9 AND 10).
RC TISSUE=Hepatoma;
RX MEDLINE=97376179; PubMed=9232351;
RA Brereton H.M., Harland M.L., Frosio M., Petronijevic T.,
RA Barrett G.J.;
RT "Novel variants of voltage-operated calcium channel alpha-1 subunit
RT transcripts in a rat liver-derived cell line: deletion in the IVS4
RT voltage sensing region.";
RL Cell Calcium 22:39-52(1997).
RN [7]
RP SEQUENCE OF 1307-1479 FROM N.A. (ISOFORM 3).
RX MEDLINE=90239020; PubMed=1692134;
RA Snutch T.P., Leonard J.P., Gilbert M.M., Lester H.A., Davidson N.;
RT "Rat brain expresses a heterogeneous family of calcium channels.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395(1990).
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE

CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D
CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), AGATOXIN-IIIA
CC PHENYALKALAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-IIIA
CC (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
CC GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=14;
CC Comment=The region sequenced in isoforms ROB3 and RKC5 is
CC identical to CACNA4;
CC Name=1; Synonyms=CACNA4A;
CC IsoId=P27732-1; Sequence=Displayed;
CC Name=2; Synonyms=CACNA4B;
CC IsoId=P27732-2; Sequence=VSP_000923, VSP_000924;
CC Name=3; Synonyms=CACH3A, RB48, RBD-55;
CC IsoId=P27732-3; Sequence=VSP_000921;
CC Name=4; Synonyms=Delta-IV-S3;
CC IsoId=P27732-4; Sequence=VSP_000919;
CC Name=5; Synonyms=Delta-IV-S4;
CC IsoId=P27732-5; Sequence=VSP_000922;
CC Name=6; Synonyms=RB9;
CC IsoId=P27732-6; Sequence=VSP_000920, VSP_000921;
CC Name=7; Synonyms=RB11;
CC IsoId=P27732-7; Sequence=VSP_000917;
CC Name=8; Synonyms=RB34;
CC IsoId=P27732-8; Sequence=VSP_000916;
CC Name=9; Synonyms=RH1;
CC IsoId=P27732-9; Sequence=VSP_000918;
CC Name=10; Synonyms=RH2;
CC IsoId=P27732-10; Sequence=VSP_000919, VSP_000922;
CC Name=11; Synonyms=RKC5;
CC IsoId=P27732-13; Sequence=Not described;
CC Name=12; Synonyms=RKC6;
CC IsoId=P27732-11; Sequence=VSP_000919;
CC Name=13; Synonyms=ROB3;
CC IsoId=P27732-14; Sequence=Not described;
CC Name=14; Synonyms=Truncated;
CC IsoId=P27732-12; Sequence=VSP_000925, VSP_000926;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PANCREATIC ISLETS AND B-
CC LYMPHOCYTES.
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; D38101; BAA07282.1; -
CC EMBL; D38102; BAA07283.1; -
CC EMBL; M57682; AAA42015.1; -
CC EMBL; U14005; AAB60515.1; -
CC EMBL; M92221; AAA40895.1; -
CC EMBL; U31772; AAA89156.1; -
CC EMBL; U49126; AAB61634.1; -


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DR EMBL; U49127; AAB61635.1; --
DR EMBL; U49128; AAB61636.1; --
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002077; Ca_channel.
DR InterPro; IPR002111; Ca_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR005446; LVDCCAlphal.
DR InterPro; IPR005452; LVDCCAlphald.
DR InterPro; IPR005820; Mchannel_nlg.
DR Pfam; PF00520; Ion_chan; 4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01630; LVDCCAlphal.
DR PRINTS; PR01636; LVDCCAlphald.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Repeat; Multigene family;
KW Calcium-binding; Phosphorylation; Alternate splicing.
FT REPEAT 112 408 I.
FT REPEAT 528 774 II.
FT REPEAT 892 1174 III.
FT REPEAT 1211 1486 IV.
FT DOMAIN 1 126 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 127 145 S1 OF REPEAT I (POTENTIAL).
FT DOMAIN 146 163 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 164 183 S2 OF REPEAT I (POTENTIAL).
FT DOMAIN 184 195 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 196 214 S3 OF REPEAT I (POTENTIAL).
FT DOMAIN 215 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 254 S4 OF REPEAT I (POTENTIAL).
FT DOMAIN 255 273 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 274 293 S5 OF REPEAT I (POTENTIAL).
FT DOMAIN 294 381 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 382 406 S6 OF REPEAT I (POTENTIAL).
FT DOMAIN 407 582 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 583 602 S1 OF REPEAT II (POTENTIAL).
FT DOMAIN 603 617 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 618 636 S2 OF REPEAT II (POTENTIAL).
FT DOMAIN 637 644 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 645 663 S3 OF REPEAT II (POTENTIAL).
FT DOMAIN 664 673 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 674 692 S4 OF REPEAT II (POTENTIAL).
FT DOMAIN 693 711 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 712 732 S5 OF REPEAT II (POTENTIAL).
FT DOMAIN 733 786 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 787 811 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 812 945 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 946 964 S1 OF REPEAT III (POTENTIAL).
FT DOMAIN 965 980 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 981 1000 S2 OF REPEAT III (POTENTIAL).

Query Match 7.4%; Score 88.5; DB 1; Length 2203;
Best Local Similarity 25.0%; Pred. No. 7.8;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy 21 VRTGTLGVWYLIINAVLLILSLALA-----DP-DYVNFSSSELG-GDFFEMDDANNCI 74
Db 934 IRVGCXKLNIHIFNLILVIMLSSAALAEEDPIRSHSFNTILGYFDYAF-----985

Qy 75 AIALSLMLICAMATYGAKORAAWIIPFCYQIFDFALNMLVAITVLIYPSNQIEYR 134
Db 986 -TAFTVEILL-KWTFCAFLHKA-----FCRNYFNL-LDMLVGVGSLV-----1027

Qy 135 QLPNPPFPDDVMSVNPCLVLIILPISILITFKG--YLISCWCNRYINGRNSDVL 192
Db 1028 ----SFGIQSSAISVVKILRVLRPLRINRAKGLKHVVQCVPVAIRTI-----GNIM 1078

Qy 193 VVVT 196
Db 1079 IVTT 1082

RESULT 14
```

```
NU2M DROMA
ID NU2M DROMA STANDARD; PRT; 274 AA.
AC P2987;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3) (Fragment).
GN ND2.
OS Drosophila mauritiana (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7226;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91088557; PubMed=2124697;
RT "Evolution of Drosophila mitochondrial DNA and the history of the
RT melanogaster subgroup.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9558-9562(1990).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M57912; AAA99050.1; --
DR FlyBase; FBgn0012512; Dmau|mt:ND2.
DR InterPro; IPR003917; NADH_oxred2.
DR InterPro; IPR003916; NADH_oxred5.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
DR PRINTS; PR01436; NADHDHGNASE2.
DR PRINTS; PR01434; NADHDHGNASES.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
FT NON TER 1
FT SEQUENCE 274 AA; 32226 MW; BB27336F8E8ED40B CRC64;

Query Match 7.3%; Score 88; DB 1; Length 274;
Best Local Similarity 21.0%; Pred. No. 1.1;
Matches 37; Conservative 29; Mismatches 56; Indels 54; Gaps 6;

Qy 28 LGVWYLIINAVLLILSLALADPDQYN-----FSS-SELGGDFEFMDANMCIAISL 80
Db 77 LNIKYLILSVILSVIIGLGLGGLNQTSLRKMAFSSINHLGW-----MLSS 122
Qy 81 LMILICAMATYGAKORAAWIIPFCYQIFDFALNMLVAITVLIYPSNQIEYR-----132
Db 123 LMI-----SSSIWLIYFFFSFLSVLTFMFNIFKLFLHQLQFSMFVSKILK 170
Qy 133 -----TRQPPNPPYRDDVMSVNPCL-----VLIILPISILITFKGYLISC 175
Db 171 FTLPNMFSLGGLPPFLGFLPKWLVIOQLTLCNQYFLLLLMMSTLITLFFYLKIC 226

RESULT 15
MTR_NEUCR
ID MTR_NEUCR STANDARD; PRT; 470 AA.
AC P38680;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE N amino acid transport system protein (Methyltryptophan resistance
DE protein).
GN MTR.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 2, 2004, 14:19:40 ; Search time 35 Seconds
(without alignments)
1666.283 Million cell updates/sec

Title: US-09-965-529-26

Perfect score: 1200

Sequence: 1 MKMVAPWTRFYSNCSCLCCH.....YDDATVNGAAKEPPPPYVSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:**
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	226	4 Q9H060	Q9H060 homo sapien
2	1200	100.0	283	4 Q9NY06	Q9NY06 homo sapien
3	1113.5	92.8	227	11 Q9IX06	Q9IX06 mus musculus
4	552.5	46.0	233	11 Q8BG66	Q8BG66 mus musculus
5	550.5	45.9	233	4 Q8BTU8	Q8BTU8 homo sapien
6	432.5	36.0	197	11 Q9CRX2	Q9CRX2 mus musculus
7	315	26.2	313	5 Q96AG6	Q96AG6 bombyx mori
8	287.5	24.0	421	5 Q8MKR3	Q8MKR3 drosophila
9	287.5	24.0	428	5 Q9SR82	Q9SR82 drosophila
10	282.5	23.5	432	5 Q9V4X3	Q9V4X3 drosophila
11	170	14.2	261	11 Q9JJ55	Q9JJ55 rattus norv
12	157	13.1	286	5 Q9BLM6	Q9BLM6 schistosoma
13	156	13.0	261	11 Q8BFZ0	Q8BFZ0 mus musculus
14	146.5	12.2	281	5 Q9U597	Q9U597 schistosoma
15	122	10.2	165	5 Q9VEW3	Q9VEW3 drosophila
16	115	9.6	236	5 Q23190	Q23190 caenorhabdi

ALIGNMENTS

RESULT 1

ID	Q9H060	PRELIMINARY;	PRT;	226 AA.
AC	Q9H060;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Hypothetical protein NP2RM1000066 (Putative integral membrane protein)			
DE	(lysosomal-associated transmembrane protein 4 beta) (Putative integral membrane transporter).			
GN	DKFP586E1124 OR LAPTMA4BETA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Uterus;			
RX	MEDLINE=11154917; PubMed=11230166;			
RA	Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,			
RA	Ansorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,			
RA	Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,			
RA	Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,			
RA	Wambutt R., Korn B., Klein M., Rouska A.,			
RT	"Towards a Catalog of Human Genes and Proteins: Sequencing and			
RT	Analysis of 500 Novel Complete Protein Coding Human cDNAs.";			
RL	Genome Res. 11:422-435(2001).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RA	Shao G., Zhou R.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RP	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RA	Strausberg R.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RP	[4]			
RP	SEQUENCE FROM N.A.			
RA	Hogue D.L.;			

17	102.5	8.5	235	5	Q17664
18	101.5	8.5	419	5	Q95Q81
19	99.5	8.3	315	16	Q92T11
20	99.5	8.3	672	2	Q04562
21	99	8.2	263	2	Q05370
22	98.5	8.2	156	12	Q9EMQ1
23	97.5	8.1	627	5	Q81J19
24	96	8.0	151	5	Q17650
25	95.5	8.0	282	11	Q9JJ42
26	94.5	7.9	240	5	Q18527
27	94	7.8	250	5	Q9VZL8
28	94	7.8	260	16	Q8E5Q4
29	93.5	7.8	221	5	Q45310
30	93.5	7.8	301	5	Q19757
31	93	7.8	1351	11	Q02789
32	91.5	7.6	185	10	Q9M878
33	91.5	7.6	1032	16	Q9A7D5
34	91	7.6	343	8	Q9Z238
35	91	7.6	3535	5	Q8IC29
36	90	7.5	161	8	Q9XN18
37	90	7.5	540	5	Q8IC17
38	89.5	7.5	237	5	Q20508
39	89.5	7.5	293	8	Q8HET6
40	89.5	7.5	341	8	Q9MGL3
41	89	7.4	241	5	Q9VLI3
42	89	7.4	297	11	Q9JKT3
43	89	7.4	382	2	Q8KN98
44	89	7.4	391	16	Q92721
45	89	7.4	1543	4	Q8WWZ4

Q17664	caenorhabdi
Q95Q81	caenorhabdi
Q92T11	rhizobium m
Q04562	saccharomyc
Q05370	actinobacil
Q9EMQ1	amsacta moo
Q81J19	plasmodium
Q17650	caenorhabdi
Q9JJ42	rattus norv
Q18527	caenorhabdi
Q9VZL8	drosophila
Q8E5Q4	streptococ
Q45310	caenorhabdi
Q19757	caenorhabdi
Q02789	mus musculu
Q9M878	arabidopsis
Q9A7D5	caulobacter
Q9Z238	trichophyto
Q8IC29	plasmodium
Q9XN18	euglena gra
Q8IC17	plasmodium
Q20508	caenorhabdi
Q8HET6	formica tru
Q9MGL3	drosophila
Q9VLI3	drosophila
Q9JKT3	mus musculu
Q8KN98	pseudomonas
Q92721	listeria in
Q8WWZ4	homo sapien

RT "Identification of a novel LAPTM cDNA."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [6]

RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,

RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahara K., Sugano S., Isegai T.;

RA "HRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL136942; CAB66876.1; -
DR EMBL; AY057051; AAL17908.1; -

DR EMBL; BC014129; AAH14129.1; -
DR EMBL; AF317417; AAK69595.1; -

DR EMBL; BC031021; AAH31021.1; -
DR EMBL; AK075326; BAC11549.1; -

DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.

KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 226 AA; 25419 MW; A3156D2F2C0DCF0B CRC64;

Query Match 100.0%; Score 1200; DB 4; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.4e-108;

Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGWYLIINAVLLILLSALADPDQYFSSSEL 60
Db 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGWYLIINAVLLILLSALADPDQYFSSSEL 60

Qy 61 GGDPEFMDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPSNIOEYIRQLPPNFPYRDDVMSVNPCTCLVLILLFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPSNIOEYIRQLPPNFPYRDDVMSVNPCTCLVLILLFISILTFKGYLISCVWNCY 180

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Best Local Similarity 100.0%; Pred. No. 1.8e-108;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGWYLIINAVLLILLSALADPDQYFSSSEL 60
Db 58 MKWVAPWTRFYSNCCLCCHVRTGTTLLGWYLIINAVLLILLSALADPDQYFSSSEL 117

Qy 61 GGDPEFMDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 118 GGDPEFMDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 177

Qy 121 TVLIYPSNIOEYIRQLPPNFPYRDDVMSVNPCTCLVLILLFISILTFKGYLISCVWNCY 180
Db 178 TVLIYPSNIOEYIRQLPPNFPYRDDVMSVNPCTCLVLILLFISILTFKGYLISCVWNCY 237

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

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QY 61 GGDFFEMDDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAI 120
RC TISSUE=Kidney;
DB 61 GGEFFEMDDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAI 120
QY 121 TVLIYVNSIQEVIROLPNPNFVRDVMNSVNTCLVLIILLFISIIITLTKGYLISCVWNCY 180
DB 121 TVLVYVNSIQEVIROLPNPNFVRDVMNSVNTCLVLIILLFISIIITLTKGYLISCVWNCY 180
QY 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDAT-VNGAAKEPPPPYVSA 226
DB 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVPSTAKEPPPPYVSA 227

RESULT 4
Q8BG66 PRELIMINARY; PRT; 233 AA.
ID Q8BG66;
AC Q8BG66;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lysosomal-associated protein transmembrane 4A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Body, Heart, and Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK075699; BAC35897.1; -.
DR EMBL; AK084515; BAC39207.1; -.
DR EMBL; AK088958; BAC40672.1; -.
SQ SEQUENCE 233 AA; 26813 MW; BP60C9722A9DFBDB CRC64;

Query Match 46.0%; Score 552.5; DB 11; Length 233;
Best Local Similarity 45.2%; Pred. No. 1e-45;
Matches 104; Conservative 44; Mismatches 61; Indels 21; Gaps 6;

QY 9 RPYNSCCLCCHVRTGTTILGWVYLIINAVVLLIILSLADPD-----QY----NFSS 57
DB 13 RPYSTRCCGCHVRTGTTILGWVYVNVNLLMAILLTVETHPNSMPAVNIQYEVIGNYIS 72
QY 58 SELGGDFEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNML 117
DB 73 SERMAD-----NACVLFAVSLVLMFISSMLVYGAISVQVGLIPFFCYRLDFVLSCL 125
QY 118 VAITVLIYVNSIQEVIROLPNPNFVRDVMNSVNTCLVLIILLFISIIITLTKGYLISCVW 177
DB 126 VAISSLTLYPRIKEYLDQI-PDPFYKDLLALDSSCLLFIVLVPFWFIIFKAYLINCWV 184
QY 178 NCYRYINGRNSDVLVY-VTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
DB 185 NCYKYINNRNVPETIAYFAFEPPOVLYPTYEMA-VKPIKEPPPPYLP 233

RESULT 5
Q8BTU8 PRELIMINARY; PRT; 233 AA.
ID Q8BTU8;
AC Q8BTU8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Lysosomal-associated protein transmembrane 4 alpha.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

QY 61 GGDFFEMDDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAI 120
RC TISSUE=Kidney;
DB 61 GGEFFEMDDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAI 120
QY 121 TVLIYVNSIQEVIROLPNPNFVRDVMNSVNTCLVLIILLFISIIITLTKGYLISCVWNCY 180
DB 121 TVLVYVNSIQEVIROLPNPNFVRDVMNSVNTCLVLIILLFISIIITLTKGYLISCVWNCY 180
QY 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDAT-VNGAAKEPPPPYVSA 226
DB 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVPSTAKEPPPPYVSA 227

RESULT 4
Q8BG66 PRELIMINARY; PRT; 233 AA.
ID Q8BG66;
AC Q8BG66;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lysosomal-associated protein transmembrane 4A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Body, Heart, and Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK075699; BAC35897.1; -.
DR EMBL; AK084515; BAC39207.1; -.
DR EMBL; AK088958; BAC40672.1; -.
SQ SEQUENCE 233 AA; 26813 MW; BP60C9722A9DFBDB CRC64;

Query Match 46.0%; Score 552.5; DB 11; Length 233;
Best Local Similarity 45.2%; Pred. No. 1e-45;
Matches 104; Conservative 44; Mismatches 61; Indels 21; Gaps 6;

QY 9 RPYNSCCLCCHVRTGTTILGWVYLIINAVVLLIILSLADPD-----QY----NFSS 57
DB 13 RPYSTRCCGCHVRTGTTILGWVYVNVNLLMAILLTVETHPNSMPAVNIQYEVIGNYIS 72
QY 58 SELGGDFEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNML 117
DB 73 SERMAD-----NACVLFAVSLVLMFISSMLVYGAISVQVGLIPFFCYRLDFVLSCL 125
QY 118 VAITVLIYVNSIQEVIROLPNPNFVRDVMNSVNTCLVLIILLFISIIITLTKGYLISCVW 177
DB 126 VAISSLTLYPRIKEYLDQI-PDPFYKDLLALDSSCLLFIVLVPFWFIIFKAYLINCWV 184
QY 178 NCYRYINGRNSDVLVY-VTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
DB 185 NCYKYINNRNVPETIAYFAFEPPOVLYPTYEMA-VKPIKEPPPPYLP 233

RESULT 5
Q8BTU8 PRELIMINARY; PRT; 233 AA.
ID Q8BTU8;
AC Q8BTU8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Lysosomal-associated protein transmembrane 4 alpha.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003158; AA03158.1; -.
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.
DR TIGRFAMs; TIGR00799; mtp; 1.
KW Transmembrane.
SQ SEQUENCE 233 AA; 26816 MW; 9BB77788B85B2E3E CRC64;

Query Match 45.9%; Score 550.5; DB 4; Length 233;
Best Local Similarity 44.8%; Pred. No. 1.6e-45;
Matches 103; Conservative 46; Mismatches 60; Indels 21; Gaps 6;

QY 9 RPYNSCCLCCHVRTGTTILGWVYLIINAVVLLIILSLADPD-----QY----NFSS 57
DB 13 RPYSTRCCGCHVRTGTTILGWVYVNVNLLMAILLTVETHPNSMPAVNIQYEVIGNYIS 72
QY 58 SELGGDFEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNML 117
DB 73 SERMAD-----NACVLFAVSLVLMFISSMLVYGAISVQVGLIPFFCYRLDFVLSCL 125
QY 118 VAITVLIYVNSIQEVIROLPNPNFVRDVMNSVNTCLVLIILLFISIIITLTKGYLISCVW 177
DB 126 VAISSLTLYPRIKEYLDQI-PDPFYKDLLALDSSCLLFIVLVPFWFIIFKAYLINCWV 184
QY 178 NCYRYINGRNSDVLVY-VTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
DB 185 NCYKYINNRNVPETIAYFAFEPPOVLYPTYEMA-VKMPEKEPPPPYLP 233

RESULT 6
Q8CRX2 PRELIMINARY; PRT; 197 AA.
ID Q8CRX2;
AC Q8CRX2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 13 days embryo head cDNA, RIKEN full-length enriched library,
DE clone:3110001N02 product:lysosomal-associated protein transmembrane
DE 4A, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai Y., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
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RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplex capillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL, AK013963; BAB29087.2; -
SQ SEQUENCE 197 AA; 22608 MW; 43CB906B0530761D CRC64;

Query Match 36.0%; Score 432.5; DB 11; Length 197;
Best Local Similarity 41.3%; Pred. No. 3.9e-34;
Matches 85; Conservative 43; Mismatches 57; Indels 21; Gaps 6;

QY 33 LIINAVVLLLSALADPD-----QY-----NFSSSELGGDFPFMDANNMCIAIAISLL 81
DB 1 MVNLLMAILTVEVTHNSPANNVQIEVIGNYSSEBMD-----NACVLFAVSVL 53
QY 82 MILICAMATYGAAYKQRAAIIIPFCYQIFDPAALMLVAITVLIYNSIQEYIROLPPNFP 141
DB 54 MFIISMLVYGAISYQVGLIPFFCYRUFDFVLSCLVAISLTYLPRIKYLQDL-PDFP 112
QY 142 YRDDVMSVNPCLVLIILFTSIIITKKGVLISCVNVCYRYINGRNSSDVLVY-VTSNDT 200
DB 113 YKDLLALDSSCLLFVILVFFVFIIFKAYLINCVMNVCYKYNINRNVPETAVYAFETPP 172
QY 201 TVLLPPYDDATVNGAAKEPPPPYVSA 226
DB 173 QYVLPTEYMA-VKPEKEPPPPYLP 197

RESULT 7
Q964G6
ID AC Q964G6 PRELIMINARY; PRT; 313 AA.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Lyosomal-associated transmembrane protein.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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RP SEQUENCE FROM N.A.
RA Hoque D.L.;
RT "Identification of a LAPTM ortholog in Bombyx mori.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF317420; AAK69598.1; -
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.
KW Transmembrane.
SQ SEQUENCE 313 AA; 34292 MW; 52CB6D97E0DB71C3 CRC64;

Query Match 26.2%; Score 315; DB 5; Length 313;
Best Local Similarity 29.0%; Pred. No. 1.6e-22;
Matches 76; Conservative 47; Mismatches 79; Indels 60; Gaps 8;

QY 15 CCLCCHVTCITILLGVWYLIINAVVLLLSALADP---DOYNFSSSELG-----GD 63
DB 18 CCFLCHVTCITILLGVWYLIINAVVLLLSALADP---DOYNFSSSELG-----GD 77
QY 64 F-----EFMDANNMCIAIAISLMLICAMATYGAAYKQRAAIIIPF 104
DB 78 VLPFLSNVETRPSYPQSASHSDHSLIYLGTMTALIMI-----YGAARGKPAVLLPF 132
QY 105 FCYQIFDPAALMLVAITVLIYNSIQEYIROLPPNFPYRDDVMSVNPCLVLIILFISI 164
DB 133 FCLQIFDFAITILTATGTCYLCRQIHAIHAE--TRRVFPRELLRLPAPALAFVVISALIV 191
QY 165 ILTFKGVLIISCVNVCYRYINGRNS--DVLVYVTSNDTV-----LL 204
DB 192 AVIIGKVCISVWRVCYKYLTMRTAAQLSLTPFVVISDGI VTSAPAPPYPOPAPDYSSLL 251
QY 205 PPYDDATVNGAAKEPPPPYVSA 226
DB 252 PDYEAA----VKOTPPPSYEA 269

RESULT 8
Q8MKR3
ID AC Q8MKR3 PRELIMINARY; PRT; 421 AA.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG14767-PA.
GN CG14767 OR CG8575.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laiko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacle D.J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacle B.J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the ENBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the ENBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the ENBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the ENBL/GenBank/DBJ databases.
DR ENBL; AB003836; AAM68833.1; -
DR FlyBase; FBgn0040777; CG14767.
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.
SQ SEQUENCE 421 AA; 46079 MW; 84EE22F2FF6799AC CRC64;

Query Match 24.0%; Score 287.5; DB 5; Length 421;
Best Local Similarity 26.8%; Pred. No. 9.9e-20;
Matches 71; Conservative 41; Mismatches 82; Indels 71; Gaps 7;

Qy 14 SCCLCCHVRGTILLGWYLLINAVLLIL-----LVCTCMIAITLMI-----YGTIK 43
Db 32 TCCFGLHVHTATLMIGLWHLFLNLIALSVLAVIWRNPEMDELEGGTHDYTVLSAPALP 91
Qy 44 --LSALADPDQY-----NFSSELGGDFEFMDANMCIA-IAISLLMLICAMATYGYK 95
Db 92 TPLSKVPPVAYRDSLSNYQNFDWGG-----LVCTCMIAITLMI-----YGTIK 136
Qy 96 QRAAWIIPFCYQIFDFALNMLVAITVLIYVNSIQEVIQRPFPNPPYRDDVMSVNPCLV 155

Query Match 24.0%; Score 287.5; DB 5; Length 421;
Best Local Similarity 26.8%; Pred. No. 9.9e-20;
Matches 71; Conservative 41; Mismatches 82; Indels 71; Gaps 7;

Qy 137 GKPSHLLPFFCLOLDFPAITTLTAAGYLCYLOAHSIIAE-SHRLPWREKLELPPPELV 195
Qy 156 LIILFISITLTKGYLISCVNVCYRYI-----NGRNSSDVLVYVTSN 198
Db 196 VVVLVFCIVFLKAYCIGIVWRCYKLTURQOHVRTLFPFLEPPTGVHSGVGTFGAER 255
Qy 199 DTTVLLPPYDDATVNGAAKEPPPPY 223
Db 256 SYSTLLPNYDEATAQYLKQAPPSPY 280

RESULT 9
Q95R82 PRELIMINARY; PRT; 428 AA.
AC Q95R82;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE SD02746P.
GN CG14767 OR CG8575.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacle B.J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnik S.;
RL Submitted (OCT-2001) to the ENBL/GenBank/DBJ databases.
DR ENBL; AY061575; AAL29123.1; -
DR FlyBase; FBgn0040777; CG14767.
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.
SQ SEQUENCE 428 AA; 47005 MW; 59F65579E88DB57D CRC64;

Query Match 24.0%; Score 287.5; DB 5; Length 428;
Best Local Similarity 26.8%; Pred. No. 1e-19;
Matches 71; Conservative 41; Mismatches 82; Indels 71; Gaps 7;

Qy 14 SCCLCCHVRGTILLGWYLLINAVLLIL-----LVCTCMIAITLMI-----YGTIK 43
Db 39 TCCFGLHVHTATLMIGLWHLFLNLIALSVLAVIWRNPEMDELEGGTHDYTVLSAPALP 98
Qy 44 --LSALADPDQY-----NFSSELGGDFEFMDANMCIA-IAISLLMLICAMATYGYK 95
Db 99 TPLSKVPPVAYRDSLSNYQNFDWGG-----LVCTCMIAITLMI-----YGTIK 143
Qy 96 QRAAWIIPFCYQIFDFALNMLVAITVLIYVNSIQEVIQRPFPNPPYRDDVMSVNPCLV 155
Db 144 GKPSHLLPFFCLOLDFPAITTLTAAGYLCYLOAHSIIAE-SHRLPWREKLELPPPELV 202
Qy 156 LIILFISITLTKGYLISCVNVCYRYI-----NGRNSSDVLVYVTSN 198
Db 203 VVVLVFCIVFLKAYCIGIVWRCYKLTURQOHVRTLFPFLEPPTGVHSGVGTFGAER 262

Query Match 24.0%; Score 287.5; DB 5; Length 421;
Best Local Similarity 26.8%; Pred. No. 9.9e-20;
Matches 71; Conservative 41; Mismatches 82; Indels 71; Gaps 7;

Qy 199 DTTVLLPPYDDATVNGAAKEPPPPY 223
Db 263 SYSTLLPNYDEATAQYLKQAPPSPY 287

RESULT 10
Q9V4X3 PRELIMINARY; PRT; 432 AA.
AC Q9V4X3; Q9V4X4.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CG14767 protein (Lysosomal-associated transmembrane protein).

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GN CG14767 OR CG8575.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Hogue D.L.;
RT "Identification of a LAPTM ortholog in Drosophila melanogaster."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM PRODUCED BY ALTERNATIVE SPLICING.
DR EMBL; AE003836; AAF59049.2; -
DR EMBL; AE003836; AAF59050.2; -
DR EMBL; AF317419; AAK69597.1; -
DR FlyBase; FBgn0040777; CG14767.
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.
KW Alternative splicing; Transmembrane.
FT VARSPLIC 1 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 432 AA; 47609 MW; ADBB0CC036EC74C4 CRC64;

Query Match 23.5%; Score 282.5; DB 5; Length 432;
Best Local Similarity 26.4%; Pred. No. 3.1e-19;
Matches 68; Conservative 40; Mismatches 97; Indels 53; Gaps 5;

Qy 14 SCCLCHVCTGTTLLGWYLIINAVLLIISALADPDQYNFSSSELGGDFEFMD-- 69
Db 39 TCCFGLVHTATLMLGLHFLNLIALSVLAVRNPEMD-----ELEGGHTDYDLISA 94

SEQUENCE FROM N.A.
PRT; 261 AA.
PRELIMINARY;
AC O9JJ55;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE GCD-10.
GN GCD-108.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192472; PubMed=11295227;
RA Origasa M., Tanaka S., Suzuki K., Tone S., Lim B., Koike T.;
RT "Activation of a Novel Microglial Gene Encoding a Lysosomal Membrane
RT Protein in Response to Neuronal Apoptosis."
RL Mol. Brain Res. 88:1-13(2001).
DR EMBL; AB046592; BAB03459.1; -
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.
DR TIGRFAMs; TIGR00799; mtp; 1.
SQ SEQUENCE 261 AA; 29631 MW; 4C2FEABCE214DDE CRC64;

Query Match 14.2%; Score 170; DB 11; Length 261;
Best Local Similarity 23.0%; Pred. No. 1.6e-08;
Matches 60; Conservative 47; Mismatches 90; Indels 64; Gaps 11;

Qy 14 SCCLCHVCTGTTLLGWYLIINAVLLI--LLSALADPDQYNFSSSELGGDFEFMDAN 71
Db 11 TCC-CFNVRVATVALAIYHIV-SVLLFIEHVVEVARGKVSRCFSK-----MPYLAD 62

SEQUENCE FROM N.A.
PRT; 286 AA.
PRELIMINARY;
AC O9BLM6;
DT 01-JUN-2001 (Tremblrel. 17, Created)

```



```
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tripanning orphan receptor.
GN TM3.
OS Schistosoma haematobium (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6185;
(1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92296361; PubMed=10366712;
RA Inal J.M.;
RT "Schistosoma TOR (trispinning orphan receptor), a novel, antigenic
RT surface receptor of the blood-dwelling, Schistosoma parasite.";
RL Biochim. Biophys. Acta 1445:283-298(1999).
DR EMBL; U57714; AAK11492.1; -
KW Receptor.
SQ SEQUENCE 286 AA; 31755 MW; A188B2046289C248 CRC64;

Query Match 13.1%; Score 157; DB 5; Length 286;
Best Local Similarity 21.6%; Pred. No. 3.1e-07;
Matches 43; Conservative 29; Mismatches 69; Indels 58; Gaps 4;

Qy 74 IATAISLLMILICAMATYGAQKRAAWIIPFCYQIFDFALNMLVAITLVIPNSIQ 133
Db IAVCVTFSLAFCCFMVHAATITRQPTLLPFFIQQVFDLIICLIHILGFMSTSDIRLVI 87
Qy 134 RQLPPNPPYRDDVMSNPTCLVLILLFISILITFKGLISCVNVCYRI----- 183
Db 88 HT-----KTGPYIKSTGTFTIILSICMMLAFKAYCLGWMWDCYKYLMLNRGNLLD 140
Qy 184 -----NGRNS-----DVLVVTNSDITVLLPP 206
Db 141 DWYSDQWHLSTFWSLRAGNSGSPNEPTRPRPTITVDPN-----LPK 196
Qy 207 YDDATVNGAAKEPPPPYVS 225
Db 197 YEDILKIRNAVAPPYICS 215

RESULT 13
Q8BFZ0 PRELIMINARY; PRT; 261 AA.
AC Q8BFZ0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lysosomal-associated protein transmembrane 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
(1)
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RC MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK089432; BAC40881.1; -
DR EMBL; AK089535; BAC40917.1; -
SQ SEQUENCE 261 AA; 29619 MW; DC4575620AB40EE5 CRC64;

Query Match 13.0%; Score 156; DB 11; Length 261;
Best Local Similarity 22.4%; Pred. No. 3.5e-07;
Matches 60; Conservative 48; Mismatches 82; Indels 78; Gaps 13;

Qy 14 SCCLCHVVTGTLIGVYLLINAVVLLILSALADPPQYVNFSSSELGDFEFDDANMC 73
Db 11 TCC-CFNIRVATIALIYHMVMS--VLLFIEHV-----EVARGKVCRRFFKPYLRMA 61

Query Match 12.2%; Score 146.5; DB 5; Length 281;
Best Local Similarity 20.5%; Pred. No. 3.2e-06;
Matches 41; Conservative 33; Mismatches 67; Indels 59; Gaps 5;

Qy 74 IATAISLLMILICAMATYGAQKRAAWIIPFCYQIFDFALNMLVAITLVIPNSIQ 133
Db IAVCVTFSLAFCCFMVHAATITRQPTLLPFFIQQVFDLIICLIHILGFMSTSDIRLMI 87
Qy 134 RQLPPNPPYRDDVMSNPTCLVLILLFISILITFKGLISCVNVCYRI----- 183
Db 88 HT-----KTGPYIKSTGTFTIILSICMMLAFKAYCLGVTWDCYKYLMLNRKSNLLD 140
Qy 184 -----NGRNS-----SDVLVVTNSDITVLLPP 206
Db 141 DWYSDQWHLSTFWSLRAGNSGSPNEPTRPRPTITVDPN-----LPK 196
Qy 207 YDD-ATVNGAAKEPPPPYVS 225
Db 197 YEDILKIPNAVAPPYICS 216

RESULT 15
Q9VEW3 PRELIMINARY; PRT; 165 AA.
AC Q9VEW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CG10311 protein (R861190p).
GN CG10311.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
```


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OM protein - protein search, using sw model

Run on: February 2, 2004, 14:15:55 ; Search time 41 Seconds
(without alignments)
874.932 Million cell updates/sec

Title: US-09-965-529-26
Perfect score: 1200
Sequence: 1 MKMVAPWTRFYSNCLCLCH.....YDDATVNGAKEPPPPYVSA 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 19Jun03.*

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- 3: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
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- 12: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
- 13: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
- 14: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
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- 19: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
- 20: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
- 21: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
- 22: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
- 23: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
- 24: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	226	21	AA194879
2	1200	100.0	226	22	ABU52920
3	1200	100.0	226	22	AA194879
4	1200	100.0	226	22	AA194879
5	1200	100.0	226	22	AA194879
6	1200	100.0	226	22	AA194879
7	1200	100.0	226	22	AA194879
8	1200	100.0	226	22	AA194879
9	1200	100.0	226	22	AA194879

10	1200	100.0	283	23	ABG96360	Human ovarian can
11	892.5	74.4	301	22	AAU30363	Novel human secret
12	769	64.1	162	23	AAE26970	Human gene 12 enco
13	769	64.1	162	23	AAE27108	Human gene 12 enco
14	769	64.1	162	24	ABU64981	Human secreted pro
15	714	59.5	137	19	AAW75240	Fragment of human
16	714	59.5	137	23	AAE27004	Human gene 12 enco
17	714	59.5	137	23	AAE27142	Human gene 12 enco
18	714	59.5	137	24	ABU65015	Human secreted pro
19	682	56.8	157	20	AAV60445	Human normal bladd
20	553.5	46.1	221	22	ABU52921	Human intracellula
21	553.5	46.1	233	23	ABU52921	Human polypeptide
22	553.5	46.1	254	21	AAE26970	Human cancer assoc
23	520	43.3	183	20	AAV60444	Human normal bladd
24	515.5	43.0	215	22	AAU12173	Human PRO3574 poly
25	515.5	43.0	215	24	ABU66571	Human PRO polypept
26	515.5	43.0	215	24	ABU66847	Human secreted/tra
27	515.5	43.0	215	24	ABU59652	Novel secreted and
28	433	36.1	117	23	ABU89228	Human polypeptide
29	417	34.8	87	19	AAW75241	Fragment of human
30	417	34.8	87	23	AAE27005	Human gene 12 enco
31	417	34.8	87	23	AAE27143	Human secreted pro
32	417	34.8	87	24	ABU5016	Human secreted pro
33	282.5	23.5	425	22	ABU5016	Drosophila melanog
34	282.5	23.5	432	22	ABU5016	Drosophila melanog
35	230.5	19.2	144	23	ABU89772	Human polypeptide
36	212	17.7	113	23	ABU89067	Human polypeptide
37	195	16.2	56	20	AAV60462	Human normal bladd
38	182.5	15.2	301	21	AAU58346	Lung cancer associ
39	175.5	14.6	262	19	AAU46577	Human haematopoiet
40	164	13.7	286	22	AAU08262	Schistosoma haemat
41	162.5	13.5	284	22	ABG72727	Novel human diagno
42	157	13.1	286	22	AAU08263	Schistosoma haemat
43	156	13.0	261	19	AAU46578	Mouse haematopoiet
44	146.5	12.2	281	22	AAU08264	Schistosoma mansoni
45	146.5	12.2	281	22	AAU08271	Schistosoma mansoni

ALIGNMENTS

RESULT 1

AA194879
ID AA194879 standard; Protein; 226 AA.

AC AA194879;

DT 12-JUN-2000 (first entry)

DE Human protein clone HP02419.

Human protein; hydrophobic domain; nutritional source; haematopoiesis; cytokine production; cell proliferation; cell differentiation; immune deficiency; infectious disease; autoimmune disorder; asthma; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; allergic reaction; osteoporosis; osteoarthritis; periodontal disease; nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury; systemic cytokine damage; tissue differentiation; reperfusion injury; coagulation disorder; myocardial infarction; inflammatory condition; septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour; nephritis; therapy.

OS Homo sapiens.

PN WO200005367-A2.

PD 03-FEB-2000.

PF 22-JUL-1999; 99WO-JP03929.

PR 24-JUL-1998; 98JP-0208820.

PR 07-AUG-1998; 98JP-0224105.

PR 25-AUG-1998; 98JP-0238116.
PR 09-SEP-1998; 98JP-0254736.
PR 29-SEP-1998; 98JP-0275505.
XX
XX (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX
XX Kato S, Kimura T;
XX WPI; 2000-182694/16.
DR
XX
XX Novel human proteins having hydrophobic domains useful for treating
PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
XX
XX Claim 1; Page 275-276; 351pp; English.
XX
XX This sequence represents a human protein of the invention, which has
CC hydrophobic domains. The DNA sequences can be used as a probe or as a
CC genetic marker. The protein can also be used as a marker, and to identify
CC potential genetic disorders. The DNA and protein can also be used as
CC nutritional sources or supplements. The protein exhibits cytokine, cell
CC proliferation, cell differentiation activities and induces production of
CC other cytokines in certain cell populations. The protein also exhibits
CC immune stimulating or immune suppressing activity. It can be used in the
CC treatment of various immune deficiencies and disorders, and to treat
CC infectious diseases caused by viral, bacterial, fungal or other
CC infections. The protein is also used for treating autoimmune disorders,
CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
CC arthritis. It is also useful in the treatment of allergic reactions and
CC conditions such as asthma, and in immune suppression after organ
CC transplantation. The protein is useful in regulation of haematopoiesis
CC and consequently in the treatment of myeloid or lymphoid cell
CC deficiencies. It is also used in compositions for tissue growth or
CC regeneration. The protein is also used in the treatment of osteoporosis
CC or osteoarthritis and in the treatment of periodontal disease and other
CC tooth repair processes. The protein is used in the treatment of nervous
CC system disorders such as Alzheimer's disease, Parkinson's disease, and
CC Huntington's disease. They are useful for protection or regeneration and
CC treatment of lung or liver fibrosis, reperfusion injury in various
CC tissues, and conditions resulting from systemic cytokine damage. They are
CC also used for promoting or inhibiting tissue differentiation. They are
CC also used as contraceptives since they exhibit activin or inhibin related
CC activities and as a fertility inducing therapeutic. They are used for
CC treating various coagulation disorders and in treatment and prevention of
CC conditions resulting from coagulation activities e.g. myocardial
CC infarction or stroke. They also act as receptors, receptor ligands or
CC inhibitors or agonists of receptor/ligand interactions. They are used to
CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
CC reperfusion injury, arthritis, and nephritis. They can be used to
CC prevent tumours.
XX
XX Sequence 226 AA;
Query Match 100.0%; Score 1200; DB 21; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFDDANMCIAISLMLILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFDDANMCIAISLMLILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCLVLIILLFISILLFKGVLISCVWCY 180
Db 121 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCLVLIILLFISILLFKGVLISCVWCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 2
ABUS2920
ID ABUS2920 standard; Protein; 226 AA.
XX
XX AC ABUS2920;
XX
XX DT 14-APR-2003 (first entry)
XX
XX Human intracellular transport and trafficking protein DKFZphut1_24ell.
DE
XX Human; gene therapy; vaccine; disease treatment; detection.
KW
XX Homo sapiens.
OS
XX WO200112859-A2.
FN
XX 22-FEB-2001.
PD
XX 18-AUG-2000; 2000WO-IB01496.
PF
XX 18-AUG-1999; 99US-0149499.
PR
XX 28-SEP-1999; 99US-0156503.
XX
XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
PA
XX Wiemann S;
PI
XX WPI; 2001-327840/34.
DR
XX N-PSDB; ABX71329.
XX
XX Nucleic acids having the sequences of clones isolated from libraries of
PT different human tissues, useful in recombinant DNA methodologies -
XX
XX Claim 21; Page 534; 1095pp; English.
XX
XX This invention describes novel polynucleotides and polypeptides isolated
CC from human cDNA libraries which can be used for gene therapy or in
CC vaccines. The polynucleotides of the invention and antibodies encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The products of the
CC invention may also be used to identify modulators of expression and
CC activity and to down regulate expression and activity. The antibodies of
CC the invention may also be used as diagnostic agents for detecting the
CC presence of polypeptides in samples. This sequence represents a
CC polypeptide described in the disclosure of the invention.
XX
XX Sequence 226 AA;
Query Match 100.0%; Score 1200; DB 22; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFDDANMCIAISLMLILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFDDANMCIAISLMLILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCLVLIILLFISILLFKGVLISCVWCY 180
Db 121 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCLVLIILLFISILLFKGVLISCVWCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 3
AAM39575

AA39575 standard; Protein; 226 AA.
AA39575;
22-OCT-2001 (first entry)
Human polypeptide SEQ ID NO 2720.
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.
Homo sapiens.
WO200153312-A1.
26-JUL-2001.
26-DEC-2000; 2000WO-US34263.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598043.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
Zhao Q, Zhou P, Goodrich R, Drmanac RT;
WPI; 2001-442253/47.
N-PSDB; AA158731.
Novel nucleic acids and polypeptides, useful for treating disorders
such as central nervous system injuries -
Example 4; SEQ ID NO 2720; 10078bp; English.
The invention relates to human nucleic acids (AA157798-AA161369) and
the encoded polypeptides (AA38642-AA42213) with nootropic,
immunosuppressant and cytostatic activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral neuropathy and
localised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilization of the activities such as: immune system suppression,
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
assays for receptor activity, arthritis and inflammation, leukaemias and
C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
specification.
Sequence 226 AA;
Query Match 100.0%; Score 1200; DB 22; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKWAPWTRFYSNCCLCCHVTRTGILLGVYLIINAVVLLILLSALADPDQYNFSSSEL 60
DB 1 MKWAPWTRFYSNCCLCCHVTRTGILLGVYLIINAVVLLILLSALADPDQYNFSSSEL 60

QY 61 GGDFFMDNDANMCIAIAISLLMILI CAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAI 120
DB 61 GGDFFMDNDANMCIAIAISLLMILI CAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAI 120
QY 121 TVLIYPNISIOEYIROLPPNPPYRDDVMSVNPTCLVLIILLFISILTFKGYLISCVWNCY 180
DB 121 TVLIYPNISIOEYIROLPPNPPYRDDVMSVNPTCLVLIILLFISILTFKGYLISCVWNCY 180
QY 181 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
DB 181 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
RESULT 4
AAB74720
ID AAB74720 standard; Protein; 226 AA.
XX AAB74720;
AC AAB74720;
DT 12-JUN-2001 (first entry)
XX Human membrane associated protein MEMAP-26.
DE Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
XX antiinflammatory; anticonvulsant; immunosuppressive; antidiarrhetic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea.
XX Homo sapiens.
OS
XX WO200112662-A2.
PN
XX 22-FEB-2001.
PD
XX 14-AUG-2000; 2000WO-US22315.
XX
XX 17-AUG-1999; 99US-0149641.
PR 09-NOV-1999; 99US-0164203.
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
PI
XX WPI; 2001-168860/17.
DR N-PSDB; AAF81766.
DR
XX Isolated polypeptide with a human membrane associated protein sequence
is useful for the diagnosis, prevention and treatment of cell
proliferative, autoimmune/inflammatory, neurological and
PT gastrointestinal disorders -
PT
XX
PS
XX Disclosure; Page 138; 173pp; English.
XX AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrhetic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
CC associated with decreased expression of functional MEMAP and antagonists
CC of MEMAP are used to treat a disease or condition associated with
CC overexpression of functional MEMAP. These disorders include cell
CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
CC disorders. The MEMAP polynucleotides and proteins are also used for the
CC diagnosis of these disorders. Specific examples of these disorders
CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
CC MEMAP proteins can be used to screen for compounds which specifically
CC bind MEMAP including antibodies, oligonucleotides, proteins and small
CC molecules. MEMAP polynucleotides can be used to prepare transgenic
CC animals which can be studied to provide information concerning human
CC disease. Anti-MEMAP antibodies are useful in immunoassays for the

CC detection of MEMAP protein and can be used as antagonists to treat or
CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
CC can be delivered to target cells with genetic abnormalities with respect
CC to the expression of MEMAP to treat or prevent a disorder associated
CC with MEMAP.

XX
SQ Sequence 226 AA;
Query Match 100.0%; Score 1200; DB 22; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.4e-125; Indels 0; Gaps 0;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYNSCCCHVTRTGILLGVYLLIINAVLLILLSALADPDQYNSFSEL 60
Db 1 MKWVAPWTRFYNSCCCHVTRTGILLGVYLLIINAVLLILLSALADPDQYNSFSEL 60
Qy 61 GGDFFMDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDPAFMLMLVAI 120
Db 61 GGDFFMDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDPAFMLMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 5
AAB88317
ID AAB88317 standard; Protein; 226 AA.
AC AAB88317;
XX
XX
DT 23-MAY-2001 (first entry)
DE Human membrane or secretory protein clone PSEC0001.
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes.

XX Homo sapiens.
XX
XX EPI067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-0114090.
XX
PR 08-JUL-1999; 99JP-0194179.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0183766.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX WPI; 2001-093989/11.
XX N-PSDB; AAF93744.
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX gene therapy or as candidate target molecules in drug development -
XX
XX Claim 1; SEQ ID 2; 609pp + CD ROM; English.
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX which encode human secretory or membrane proteins represented by
XX AAB88317 - AAB88419. Included in the invention are primers
XX AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
XX cDNA sequences of the invention. The invention also includes methods for
XX the production of antibodies directed against the proteins, and cDNA
XX sequences, which can be used in vaccines. The polynucleotide sequences

CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantify the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies and antagonists may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay
CC (ELISA)). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.

XX
SQ Sequence 226 AA;

Query Match 100.0%; Score 1200; DB 22; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCCHVTRTGILLGVYLLIINAVLLILLSALADPDQYNSFSEL 60
Db 1 MKWVAPWTRFYNSCCCHVTRTGILLGVYLLIINAVLLILLSALADPDQYNSFSEL 60
Qy 61 GGDFFMDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDPAFMLMLVAI 120
Db 61 GGDFFMDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDPAFMLMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 6
AAB889618
ID AAB889618 standard; Protein; 226 AA.

XX
XX AC AAB889618;
XX
XX 24-MAY-2002 (first entry)
XX
XX Human polypeptide SEQ ID NO 1994.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein.
XX
XX Homo sapiens.
XX
XX WO200190304-A2.
XX
XX 29-NOV-2001.
XX
XX 18-MAY-2001; 2001WO-US16450.
XX
XX 19-MAY-2000; 2000US-205515P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX WPI; 2002-122018/16.
XX N-PSDB; ABL90027.
XX

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -
XX
XX
XX Claim 11; SEQ ID NO 1994; 2081pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AB89449-AB89453) and proteins
CC (AB89040-AB89044) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX

XX Sequence 226 AA;

Query Match 100.0%; Score 1200; DB 23; Length 226;

Best Local Similarity 100.0%; Pred. No. 2.4e-125;

Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPNSIOEYIRQLPFPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPNSIOEYIRQLPFPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226

RESULT 7

ABU56591

ID ABU56591 standard; Protein; 226 AA.

XX AC ABU56591;

XX

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polypeptide #184.

XX

Lung cancer-associated polypeptide; cytostatic; emphysema;
KW anti-inflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX WO200286443-A2.

XX

PD 31-OCT-2002.

XX

PF 18-APR-2002; 2002WO-US12476.

XX 18-APR-2001; 2001US-284770P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-339245P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX
XX (EOSB-) BOS BIOTECHNOLOGY INC.

XX Aziz N, Murray R;

XX WPI; 2003-093161/08.

XX DR N-PSDB; ABX76320.

XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -

XX Claim 27; Page 327; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pneumonia, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
CC polypeptides of the invention.

XX Sequence 226 AA;

Query Match 100.0%; Score 1200; DB 24; Length 226;

Best Local Similarity 100.0%; Pred. No. 2.4e-125;

Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPNSIOEYIRQLPFPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPNSIOEYIRQLPFPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226

RESULT 8

AAU41361

ID AAU41361 standard; Protein; 231 AA.

XX AC AAU41361;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 6292.

XX Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598048.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AAI60517.

XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

XX Example 2; SEQ ID NO 6292; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and

CC the encoded polypeptides (AAM38642-AAM42213) with nontropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activity, chemotactic/chemokinetic activity, haemostatic

CC Activin/inhibin activity, cancer diagnosis and therapy, drug screening,

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

XX SQ Sequence 231 AA;

Query Match 100.0%; Score 1200; DB 22; Length 231;

Best Local Similarity 100.0%; Pred. No. 2.4e-125;

Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKWAPWTFYNSNCLCHVTRTGILGVWYLIINAVVLLTLLSALADPPQYNFSSSEL 60

DB 6 MKWAPWTFYNSNCLCHVTRTGILGVWYLIINAVVLLTLLSALADPPQYNFSSSEL 65

QY 61 GGDFFEMDDANNCIAAISLMLILCAMATYGAYKQRAWIIPFCYQIFDFAIIMLVAI 120

DB 66 GGDFFEMDDANNCIAAISLMLILCAMATYGAYKQRAWIIPFCYQIFDFAIIMLVAI 125

QY 121 TVLIYPNSIQEYIROLPPNFPYRDDVMVSNPTCLVLIILTFKGLVISCWVNCY 180

Db 126 TVLIYPNSIQEYIROLPPNFPYRDDVMVSNPTCLVLIILTFKGLVISCWVNCY 185

QY 181 RYINGRNSSDLVVYVTSNDTIVLLPPYDDATVNGAAKEPPPPYVSA 226

Db 186 RYINGRNSSDLVVYVTSNDTIVLLPPYDDATVNGAAKEPPPPYVSA 231

RESULT 9

ABP64704

ID ABP64704 standard; Protein; 283 AA.

XX ABP64704;

AC ABP64704;

XX 25-FEB-2003 (first entry)

DT DT

XX Human protein SEQ ID 364.

DB Human; expressed sequence tag; EST;

XX haematopoietic disorder; central nervous system disease; viral infection;

KW peripheral nervous system disease; non-healing wound; infectious disease;

KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;

KW fungal infection; autoimmune disorder; coagulation disorder; nontropic;

KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;

KW cytostatic; haemostatic; virucide; antibacterial; fungicide;

KW immunostimulant; cerebroprotective.

XX Homo sapiens.

OS WO200259260-A2.

XX 01-AUG-2002.

XX 16-NOV-2001; 2001WO-US42950.

XX 17-NOV-2000; 2000US-0714936.

PR (HYSE-) HYSEQ INC.

XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;

PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;

XX WPI; 2002-590824/63.

DR N-PSDB; ABQ99290.

XX New isolated polynucleotide, useful in research, diagnostic or

PT therapeutic methods, e.g. preventing or treating disorders involving

PT aberrant protein expression or biological activity -

XX Claim 20; SEQ ID 364; 394pp; English.

XX The present invention relates to novel human coding sequences

CC (ABQ99268-ABQ99608) and proteins (ABP64682-ABP65022). The sequences are

CC useful in therapeutic, diagnostic and research methods. The

CC polynucleotides may be used in the field of molecular biology as

CC hybridisation probes, primers for PCR, for chromosome and gene mapping,

CC for the recombinant production of protein, or in generation of anti-sense

CC DNA or RNA. The polynucleotides are useful in diagnostics as expressed

CC sequence tags (ESTs) for identifying expressed genes or for physical

CC mapping of the human genome. The proteins may be used as molecular weight

CC markers, or as nutritional sources or supplements. The proteins may be

CC used to maintain and expand cell population in a totipotential or

CC pluripotential state useful for re-engineering damaged or diseased

CC tissues, transplantation, manufacture of bio-pharmaceuticals or the

CC development of bio-sensors. The polynucleotides and proteins are useful

CC for preventing, treating or ameliorating disorders involving aberrant

CC protein expression or biological activity, e.g. haematopoietic disorders,

CC central/peripheral nervous system diseases, mechanical and traumatic

CC disorders, non-healing wounds, immune deficiencies and disorders,

CC infectious diseases caused by viral, bacterial or fungal infection,

CC autoimmune disorders, allergic reactions and conditions, coagulation

CC disorders, or cancer. The polynucleotide sequences of the invention were

CC assembled from ESTs isolated mainly by sequencing by hybridisation, and

CC in some cases, sequences obtained from one or more public databases.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 283 AA;
Query Match 100.0%; Score 1200; DB 23; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.1e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVLLILLSALADPDQYNSSEL 60
Dy 58 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVLLILLSALADPDQYNSSEL 117
Qy 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIYDFALNMLVAI 120
Dy 118 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIYDFALNMLVAI 177
Qy 121 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLILFISILTFKGYLISCVNVCY 180
Dy 178 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLILFISILTFKGYLISCVNVCY 237
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Dy 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

RESULT 10

ABG96360
ID ABG96360 standard; Protein; 283 AA.

XX AC ABG96360;
XX DT 11-DEC-2002 (first entry)
XX DE Human ovarian cancer marker OV53.
XX KW Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW central nervous system disorder; bacterial meningitis; viral meningitis;
KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW brain herniation; inflammation; encephalitis; testicular disorder;
KW nontuberculous granulomatous orchitis; connective tissue disorder;
KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW histological type; carcinogenic; ovarian cancer marker.
XX OS Homo sapiens.
XX PN WO200271928-A2.
XX PD 19-SEP-2002.
XX PF 14-MAR-2002; 2002WO-US07826.
XX PR 14-MAR-2001; 2001US-276025P.
PR 14-MAR-2001; 2001US-276026P.
PR 10-AUG-2001; 2001US-311732P.
PR 19-SEP-2001; 2001US-323580P.
PR 26-SEP-2001; 2001US-324967P.
PR 26-SEP-2001; 2001US-325102P.
PR 26-SEP-2001; 2001US-325149P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;
PI Baer RC, Lu K, Schmandt RE, Zhao X, Glatt K;
XX DR WPI; 2002-723277/78.
DR N-P8DB; ABS76456.
XX PT Assessing whether a patient is afflicted with ovarian cancer, useful in
PT assessing the stage or progression of the disease, comprises comparing
PT the expression level of a cancer marker in a sample from a patient and

PT from a non cancer patient -

XX Disclosure; Page 296-297; 48lpp; English.

XX CC The present invention relates to a new method for assessing whether a
CC patient is afflicted with ovarian cancer. The method involves comparing
CC the expression level of a marker in a patient sample and the normal level
CC of expression of the marker in a control non-ovarian cancer sample, where
CC the marker is selected from 363 cancer markers described in the
CC specification. The method of the invention is useful in diagnosing or
CC characterising cancer, in detecting the presence of cancer as early as
CC possible, and the recurrence of ovarian cancer. The method may also be of
CC particular use with patients having an enhanced risk of developing
CC ovarian cancer (e.g. patients having a familial history of ovarian
CC cancer). The cancer markers may be used in the management and treatment
CC of e.g. brain and central nervous system disorders (e.g. bacterial and
CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain
CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
CC inflammations (e.g. bacterial or viral meningitis or encephalitis),
CC testicular disorders (e.g. nontuberculous granulomatous orchitis),
CC connective tissue disorders, or heart disorders (e.g. ischaemic heart
CC disease or atherosclerosis). The compositions and methods may also be
CC used in assessing the histological type of neoplasm associated with
CC ovarian cancer, monitoring the progression of ovarian cancer,
CC determining whether ovarian cancer has metastasized or is likely to
CC metastasize, selecting a composition for inhibiting ovarian cancer,
CC assessing the ovarian carcinogenic potential of a compound, or
CC inhibiting ovarian cancer or at risk of developing ovarian cancer. The
CC present amino acid sequence represents one of the ovarian cancer markers
CC described in the invention.

XX SQ Sequence 283 AA;

Query Match 100.0%; Score 1200; DB 23; Length 283;

Best Local Similarity 100.0%; Pred. No. 3.1e-125;

Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVLLILLSALADPDQYNSSEL 60
Dy 58 MKWVAPWTRFYSNCCLCCHVRTGTTLLGVWYLIINAVLLILLSALADPDQYNSSEL 117
Qy 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIYDFALNMLVAI 120
Dy 118 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIYDFALNMLVAI 177
Qy 121 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLILFISILTFKGYLISCVNVCY 180
Dy 178 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLILFISILTFKGYLISCVNVCY 237
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Dy 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

RESULT 11

AAU30363
ID AAU30363 standard; Protein; 301 AA.

XX AC AAU30363;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #854.

XX KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

CC secreted protein of the invention.

XX Sequence 162 AA;
SQ
Query Match 64.1%; Score 769; DB 23; Length 162;
Best Local Similarity 99.3%; Pred. No. 1.7e-77;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKWVAPTRFYNSCCCHVTRTGILLGVWYLIINAVVLLILSALADPPQYNFSSSEL 60
Db 1 MKWVAPTRFYNSCCCHVTRTGILLGVWYLIINAVVLLILSALADPPQYNFSSSEL 60
Qy 61 GGDPEFMDANNCIAAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDPAFMLMLVAI 120
Db 61 GGDPEFMDANNCIAAISLLMILICAMATYGAYKQRAAGIIPFCYQIFDPAFMLMLVAI 120
Qy 121 TVLIYPSIQEYIRQLPFPNPPYRDDVM 147
Db 121 TVLIYPSIQEYIRQLPFPNPPYRDDVM 147

RESULT 13

AAE27108

ID AAE27108 standard; Protein; 162 AA.

XX AC AAE27108;

XX DT 13-DEC-2002 (first entry)

XX DE Human gene 12 encoded secreted protein HTEBY84, SEQ ID NO:63.

XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnery.

XX OS Homo sapiens.

XX FN US2002076756-A1.

XX PD 20-JUN-2002.

XX PF 11-MAY-2001; 2001US-0853161.

XX PR 02-FEB-2001; 2001US-265583P.

XX PA (RUBE/) RUBEN S M.

XX PA (ROSE/) ROSEN C A.

XX PA (LIYY/) LI Y.

XX PA (ZENG/) ZENG Z.

XX PA (KYAW/) KYAW H.

XX PA (FISC/) FISCHER C L.

XX PA (LIH/) LI H.

XX PA (SOPP/) SOPPET D R.

XX PA (GENT/) GENTZ R L.

XX PA (WEI/) WEI Y.

XX PA (MOOR/) MOORE P A.

XX PA (YOUN/) YOUNG P E.

XX PA (GREE/) GREENE J M.

XX PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

PI Ferrie AM;

XX WPI; 2002-574454/61.

DR N-PSDB; AAD44865.

XX

PT New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
XX and as food additives or preservatives

XX Claim 11; Page 178; 209pp; English.

XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein of the invention.

XX Sequence 162 AA;

Query Match 64.1%; Score 769; DB 23; Length 162;

Best Local Similarity 99.3%; Pred. No. 1.7e-77;

Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKWVAPTRFYNSCCCHVTRTGILLGVWYLIINAVVLLILSALADPPQYNFSSSEL 60

Db 1 MKWVAPTRFYNSCCCHVTRTGILLGVWYLIINAVVLLILSALADPPQYNFSSSEL 60

Qy 61 GGDPEFMDANNCIAAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDPAFMLMLVAI 120

Db 61 GGDPEFMDANNCIAAISLLMILICAMATYGAYKQRAAGIIPFCYQIFDPAFMLMLVAI 120

Qy 121 TVLIYPSIQEYIRQLPFPNPPYRDDVM 147

Db 121 TVLIYPSIQEYIRQLPFPNPPYRDDVM 147

RESULT 14

ABU64981

ID ABU64981 standard; Protein; 162 AA.

XX AC ABU64981;

XX DT 15-MAY-2003 (first entry)

XX DE Human secreted protein gene 12, protein #1.

XX Secreted protein; immunodeficiency; multiple sclerosis;
KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
KW blood-related disorder; thrombosis; acute glomerulonephritis; renal disorder;
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
KW endocrine disorder; liver disease; reproductive system disorder;
KW endometriosis; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
KW body height; hair colour; human.

XX OS Homo sapiens.

XX

XX Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
PI Wei YF, Young PE, Zeng Z;
XX WPI; 1998-520811/44.
DR N-PSDB; AAV34297.
XX
XX Isolated human poly:nucleotide(s) encoding secretory peptide(s) -
PT used to develop products for the diagnosis and treatment of e.g.
PT inflammation, cancers, CNS disorders or immune system disorders
XX
XX Disclosure; Page 14; 20pp; English.
XX
XX This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule designated Gene 12 (AAV34297). The gene
CC can be used to generate fusion proteins by linking to the gene to a
CC human immunoglobulin Fc portion (e.g. AAV34277) for increasing the
CC stability of the fused protein as compared to the human protein only.
CC The invention relates to 28 novel genes and their fragments (nucleic
CC acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 28
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34286 for described uses).
XX
SQ Sequence 137 AA;
Query Match 59.5%; Score 714; DB 19; Length 137;
Best Local Similarity 99.3%; Pred. No. 1.9e-71;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 RFYSNSCLCCHVRTGTTLLGWYLLINAVVLLILLSALADPDQYNFSSSELGGDFPMD 60
Qy 69 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYPNS 128
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 DANMCIAIAISLLMILICAMATYGAYKORAAAGIIPFCYQIFDFALNMLVAITVLIYPNS 120
Qy 129 IQEYIRQLPPNPPYRDD 145
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 IQEYIRQLPPNPPYRDD 137

Search completed: February 2, 2004, 14:21:52
Job time : 43 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2004, 14:23:16 ; Search time 33 Seconds
(without alignments)

1423.280 Million cell updates/sec

Title: US-09-965-529-26

Perfect score:

Sequence: 1 MKMVA PWTRFYNSCCLCH.....YDDATVNGAAKEPPPPYVSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB length: 2000000000
Maximum DB length: 2000000000

post-processing: Minimum Match 0%

2000 Processing: Minimum Match 0% Maximum Match 100%

Maximum MATCH 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/pdata/1/pubaa/FCI_NEW PUB.pcp.*
3: /cgn2_6/pdata/1/pubaa/US06 NEW PUB.pcp.*
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8: /cgn2_6/pdata/1/pubaa/US08 PUBCOMB.pcp.*
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12: /cgn2_6/pdata/1/pubaa/US09 NEW PUB.pcp.*
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14: /cgn2_6/pdata/1/pubaa/US10B PUBCOMB.pcp.*
15: /cgn2_6/pdata/1/pubaa/US10C PUBCOMB.pcp.*
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18: /cgn2_6/pdata/1/pubaa/US60 NEW PUB.pcp.*
19: /cgn2_6/pdata/1/pubaa/US60 PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			Description	
	Score	Match	Length	ID	Description
1	1200	100.0	226	10	US-09-965-529-26
2	1200	100.0	226	11	US-09-969-680A-26
3	1200	100.0	226	12	US-10-264-237-1994
4	1200	100.0	283	12	US-10-301-822-99
5	1200	100.0	283	15	US-10-037-340-175
6	769	64.1	162	9	US-09-853-161-63
7	769	64.1	162	9	US-09-852-659A-63
8	769	64.1	162	10	US-09-852-797-63
9	714	59.5	137	9	US-09-852-161-97
10	714	59.5	137	9	US-09-852-659A-97
11	714	59.5	137	10	US-09-852-797-97
12	553.5	46.1	233	12	US-10-376-564-12
13	553.5	46.1	233	12	US-10-264-237-2149
14	553.5	46.1	254	9	US-09-925-301-1268
15	541.5	45.1	233	12	US-10-376-564-11

16	515.5	43.0	215	12	US-10-137-870-4	Sequence 4, Appli
17	515.5	43.0	215	12	US-10-140-018-4	Sequence 4, Appli
18	515.5	43.0	215	12	US-10-140-021-4	Sequence 4, Appli
19	515.5	43.0	215	12	US-10-140-274-4	Sequence 4, Appli
20	515.5	43.0	215	12	US-10-140-471-4	Sequence 4, Appli
21	515.5	43.0	215	12	US-10-140-807-4	Sequence 4, Appli
22	515.5	43.0	215	12	US-10-140-922-4	Sequence 4, Appli
23	515.5	43.0	215	12	US-10-140-924-4	Sequence 4, Appli
24	515.5	43.0	215	12	US-10-140-926-4	Sequence 4, Appli
25	515.5	43.0	215	12	US-10-141-698-4	Sequence 4, Appli
26	515.5	43.0	215	12	US-10-141-702-4	Sequence 4, Appli
27	515.5	43.0	215	12	US-10-141-704-4	Sequence 4, Appli
28	515.5	43.0	215	12	US-10-142-421-4	Sequence 4, Appli
29	515.5	43.0	215	12	US-10-142-432-4	Sequence 4, Appli
30	515.5	43.0	215	12	US-10-142-767-4	Sequence 4, Appli
31	515.5	43.0	215	12	US-10-143-033-4	Sequence 4, Appli
32	515.5	43.0	215	12	US-10-144-994-4	Sequence 4, Appli
33	515.5	43.0	215	12	US-10-145-628-4	Sequence 4, Appli
34	515.5	43.0	215	12	US-10-145-631-4	Sequence 4, Appli
35	515.5	43.0	215	12	US-10-145-633-4	Sequence 4, Appli
36	515.5	43.0	215	12	US-10-145-746-4	Sequence 4, Appli
37	515.5	43.0	215	12	US-10-145-748-4	Sequence 4, Appli
38	515.5	43.0	215	12	US-10-145-823-4	Sequence 4, Appli
39	515.5	43.0	215	12	US-10-145-826-4	Sequence 4, Appli
40	515.5	43.0	215	12	US-10-145-870-4	Sequence 4, Appli
41	515.5	43.0	215	12	US-10-145-876-4	Sequence 4, Appli
42	515.5	43.0	215	12	US-10-145-876-4	Sequence 4, Appli
43	515.5	43.0	215	12	US-10-146-724-4	Sequence 4, Appli
44	515.5	43.0	215	12	US-10-146-725-4	Sequence 4, Appli
45	515.5	43.0	215	12	US-10-146-795-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

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US-09-365-529-26
; Sequence 26, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yaida
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyrng Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PE-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 26
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 2795577CD1
US-09-965-529-26

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Query Match	100.0%;	Score 1200;	DB 10;	Length 226;
Best Local Similarity	100.0%;	Pred. No. 1.5e-115;		
Matches 226:	Conservative	0;	Mismatches 0;	Indels 0;
	Gaps	0;		

1 MKMVA PWTFVYNSCCI.CCHVRTGTTI.I.GVWYI.I.TNAVVI.I.II.I.SAI.ADDPOYNFSSSEL 60

QY I M R T V A F W K R F I S N S C C E C C H V K R I G I T T E U G V W I D I I N A V V D U I D E S A T A D F D Q I N I S S S E L 00

Qy 1 MKWVAPWTRFYSNCCCLCHVRTGTTILGVWYLIINAVVLLILSALADPDQYNFSSSEL 60
Db 58 MKWVAPWTRFYSNCCCLCHVRTGTTILGVWYLIINAVVLLILSALADPDQYNFSSSEL 117
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Qy 121 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCTCLVLIILFISILITPKGYLISCVWNCY 180
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Qy 121 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCTCLVLIILFISILITPKGYLISCVWNCY 180
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Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 178 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCTCLVLIILFISILITPKGYLISCVWNCY 237
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

RESULT 5

US-10-097-340-175
; Sequence 175, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAWATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-175
Query Match 100.0%; Score 1200; DB 15; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCCLCHVRTGTTILGVWYLIINAVVLLILSALADPDQYNFSSSEL 60
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Qy 61 GGDFEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
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Db 178 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCTCLVLIILFISILITPKGYLISCVWNCY 237
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

RESULT 6

US-09-853-161-63
; Sequence 63, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/285,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-63

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Best Local Similarity 99.3%; Pred. No. 2.6e-71;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-852-797-63
; Query Match 64.1%; Score 769; DB 9; Length 162;
; Best Local Similarity 99.3%; Pred. No. 2.6e-71;
; Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 61 GGDFFEMDDANMCIAISLLMILICAMATYGAYKQRAAGIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPNSIQEYIRQLPFPYRDDVM 147
Db 121 TVLIYPNSIQEYIRQLPFPYRDDVM 147
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US-09-852-797-63
; Sequence 63, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
US-09-852-659A-63
; Query Match 64.1%; Score 769; DB 9; Length 162;
; Best Local Similarity 99.3%; Pred. No. 2.6e-71;
; Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGWYLIINAVVLLILLSALADPDQYNFSSSEL 60
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Db 61 GGDFFEMDDANMCIAISLLMILICAMATYGAYKQRAAGIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPNSIQEYIRQLPFPYRDDVM 147
Db 121 TVLIYPNSIQEYIRQLPFPYRDDVM 147
RESULT 9
US-09-853-161-97
; Sequence 97, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
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; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 97
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-97

Query Match      59.5%; Score 714; DB 9; Length 137;
Best Local Similarity 99.3%; Pred. No. 9.7e-66;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 68
Db 1 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 60

Qy 69 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 128
Db 61 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 120

Qy 129 IQEYIROLPPNFPYRDD 145
Db 121 IQEYIROLPPNFPYRDD 137

RESULT 10
US-09-852-659A-97
; Sequence 97, Application US/09853659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 97
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-97

Query Match      59.5%; Score 714; DB 9; Length 137;
Best Local Similarity 99.3%; Pred. No. 9.7e-66;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 68
Db 1 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 60

Qy 69 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 128
Db 61 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 120

Qy 129 IQEYIROLPPNFPYRDD 145
Db 121 IQEYIROLPPNFPYRDD 137

RESULT 11
US-09-852-797-97
; Sequence 97, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 97
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-97

Query Match      59.5%; Score 714; DB 10; Length 137;
Best Local Similarity 99.3%; Pred. No. 9.7e-66;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 68
Db 1 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 60

Qy 69 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 128
Db 61 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 120

Qy 129 IQEYIROLPPNFPYRDD 145
Db 121 IQEYIROLPPNFPYRDD 137
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RESULT 12
US-10-376-564-12
; Sequence 12, Application US/10376564
; Publication No. US20030180302A1
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckhard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jörn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014003
; CURRENT APPLICATION NUMBER: US/10/376,564
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 09/886,319
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 100 30 149.5-41
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-376-564-12

Query Match 46.1%; Score 553.5; DB 12; Length 233;
Best Local Similarity 45.2%; Pred. No. 6.3e-49;
Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;

QY 9 RFYNSCCLCHVRTGTLIGVWYLIINAVVLLILLSALADPD-----QY-----NFSS 57
DB 13 RFYSTRCCGCHVRTGTIIIGTWVWVNLMAILLTVETHPNMSPAVNIQYEVIGNYS 72
QY 58 SELGGDFEFMDANMCIAISLMLILICAMATYGAQKRAAWIIPFCYQIFDFALNML 117
DB 73 SERMAD-----NACVLFAVSVMFTISSMLVGYAISYQVGMILPFCYRLDFVLSCL 125
QY 118 VAITVLIYPNISIOEYIRQLPNPFRDDVMSVNPCTCLVLIILLFISILITFKGYLISCVW 177
DB 126 VAISSTLYLPRIKEYLDQL-PDPFYKDDLLALDSSCLLFVLVFFALFIIFKAYLINCVW 184
QY 178 NCYRYINGRNSSDVLVY-VTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
DB 185 NCYKYNRNVPETAVYPAFAAPPQYVLPYEMA-VKMPEKEPPPPYVSA 233

RESULT 14
US-09-925-301-1268
; Sequence 1268, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1268

Query Match 46.1%; Score 553.5; DB 9; Length 254;
Best Local Similarity 45.2%; Pred. No. 6.9e-49;
Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;

QY 9 RFYNSCCLCHVRTGTLIGVWYLIINAVVLLILLSALADPD-----QY-----NFSS 57
DB 34 RFYSTRCCGCHVRTGTIIIGTWVWVNLMAILLTVETHPNMSPAVNIQYEVIGNYS 93
QY 58 SELGGDFEFMDANMCIAISLMLILICAMATYGAQKRAAWIIPFCYQIFDFALNML 117
DB 94 SERMAD-----NACVLFAVSVMFTISSMLVGYAISYQVGMILPFCYRLDFVLSCL 146
QY 118 VAITVLIYPNISIOEYIRQLPNPFRDDVMSVNPCTCLVLIILLFISILITFKGYLISCVW 177
DB 147 VAISSTLYLPRIKEYLDQL-PDPFYKDDLLALDSSCLLFVLVFFALFIIFKAYLINCVW 205
QY 178 NCYRYINGRNSSDVLVY-VTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
DB 206 NCYKYNRNVPETAVYPAFAAPPQYVLPYEMA-VKMPEKEPPPPYVSA 254

RESULT 15
US-10-376-564-11
; Sequence 11, Application US/10376564
; Publication No. US20030180302A1
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckhard
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